

UPAP-0287

IN THE UNITED STATES RECEIVING OFFICE
Before the United States Receiving Office
for the Patent Cooperation Treaty

In re application of: **Velpandi AYYAVOO; Thanadavarayan
NAGASHUNMUGAM and David B. WEINER**

International Application No.: **PCT/US98/19478**

International Filing Date: **18 September 1998**

Title: **ATTENUATED VIF DNA IMMUNIZATION CASSETTES FOR GENETIC VACCINES**

Assistant Commissioner for Patents
BOX PCT DO/EO/US
Washington, DC 20231

TRANSMITTAL LETTER SUBMITTING SEQUENCE LISTING

Applicant submits herewith the Sequence Listing in written (32 sheets) and computer readable form, the contents of which are the same.

The enclosed Sequence Listing does not go beyond the disclosure in the international application as filed.

Respectfully submitted,



Paul K. Legaard
Registration No. 38,534

/vc

Enc.: 1 Diskette; 32 sheets sequence listing
Date: 29 February 2000
WOODCOCK WASHBURN KURTZ
MACKIEWICZ & NORRIS
One Liberty Place - 46th Floor
Philadelphia, PA 19103
(215) 568-3100

SEQUENCE LISTING

<110> Ayyavoo, Velpandi

Nagashunmugam, Thandavarayan

Weiner, David B.

University of Pennsylvania

<120> ATTENUATED VIF DNA IMMUNIZATION CASSETTES FOR GENETIC
VACCINES

<130> UPAP-0263

<140> HEREWITH

<141> 1998-09-18

<160> 46

<170> PatentIn Ver. 2.0

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<211> 190

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Met Glu Asn Arg Trp Gln Val Met Ile Val Trp Gln Val Asp Arg Met

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Arg Ile Arg Thr Trp Asn Ser Leu Val Lys His His Met Tyr Val Ser

20

25

30

Lys Lys Ala Arg Trp Phe Tyr Arg His His Tyr Glu Ser Pro His Pro

35

40

45

Lys Val Ser Ser Glu Val His Ile Pro Leu Gly Asp Ala Arg Leu Glu

50

55

60

Thr Thr Thr Tyr Trp Gly Leu His Gly Glu Arg Asp Trp His Leu Gly

65

70

75

80

Gln Gly Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr Gln Val
85 90 95

Asp Pro Asp Leu Ala Asp Gln Leu Ile His Leu Tyr Tyr Phe Asp Cys
100 105 110

Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly Tyr Arg Val Ser
115 120 125

Pro Arg Cys Glu Tyr Gln Ala Gly His Asn Lys Val Gly Ser Leu Gln
130 135 140

Tyr Leu Ala Leu Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys Pro Pro
145 150 155 160

Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys Pro Gln
165 170 175

Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His
180 185 190

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gaaagcttat ggaaacaga tggcag 26

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 1 5 10 15

Arg Ile Arg Thr Trp Asn Ser Leu Val Lys Tyr His Met Tyr Ser Lys
 20 25 30

Lys Ala Arg Glu Trp Phe Tyr His His Tyr Gln Ser Pro His Pro Lys
 35 40 45

Val Ser Ser Glu Val His Ile Pro Leu Glu Asp Ala Arg Leu Glu Ile
 50 55 60

Thr Ser Phe Trp Gly Leu His Thr Gly Glu Arg Asp Trp His Leu Gly
 65 70 75 80

Gln Gly Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr His Val
 85 90 95

Asp Pro Asp Leu Ala Asp Gln Leu Ile His Leu Tyr Tyr Phe Asp Cys
 100 105 110

Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly His Arg Val Ser
 115 120 125

Pro Arg Cys Glu Tyr Arg Ala Gly His Ser Lys Val Gly Ser Leu Gln
 130 135 140

Tyr Leu Ala Ile Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys Pro Pro
 145 150 155 160

Leu Ala Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys Pro Gln
 165 170 175

Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His
 180 185 190

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Arg Ile Arg Thr Trp Asn Ser Leu Val Lys Tyr His Met Tyr Arg Ser
 20 25 30

Lys Lys Ala Arg Glu Trp Phe Tyr Arg His His Tyr Gln Ser Pro His
 35 40 45

Pro Arg Val Ser Ser Glu Val His Ile Pro Leu Glu Asp Ala Arg Leu
 50 55 60

Glu Ile Thr Thr Tyr Trp Gly Leu His Thr Gly Glu Arg Asp Trp His
 65 70 75 80

Leu Gly Gln Gly Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr
 85 90 95

Gln Val Asp Pro Asp Leu Ala Asp Gln Leu Ile His Leu Tyr Tyr Phe
 100 105 110

Asp Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly His Arg
 115 120 125

Val Ser Pro Arg Cys Glu Tyr Arg Ala Gly His Ser Lys Val Gly Ser
 130 135 140

Leu Gln Tyr Leu Ala Ile Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys
 145 150 155 160

Pro Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys
 165 170 175

Pro Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His
 180 185 190

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Met Glu Asn Arg Trp Gln Val Met Ile Val Trp Gln Val Asp Arg Met
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Arg Ile Arg Thr Trp Asn Ser Leu Val Lys Tyr His Met Tyr Arg Ser
 20 25 30

Lys Lys Ala Arg Glu Trp Phe Tyr Arg His His Tyr Gln Ser Pro His
 35 40 45

Pro Lys Val Ser Ser Glu Val His Ile Pro Leu Glu Asp Ala Arg Leu
 50 55 60

Glu Thr Thr Thr Tyr Trp Gly Leu His Thr Gly Glu Arg Asp Trp His
 65 70 75 80

Leu Gly Gln Gly Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr
 85 90 95

Gln Val Asp Pro Asp Leu Ala Asp Gln Leu Ile His Leu Tyr Tyr Phe
 100 105 110

Asp Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly His Arg
 115 120 125

Val Ser Pro Arg Cys Glu Tyr Arg Ala Gly His Ser Lys Val Gly Ser
 130 135 140

Leu Gln Tyr Leu Ala Ile Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys
 145 150 155 160

Pro Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys
 165 170 175

Pro Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His
 180 185 190

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Met Glu Asn Arg Trp Gln Val Met Ile Val Trp Gln Val Asp Arg Met

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Arg Ile Arg Thr Trp Asn Ser Leu Val Thr Tyr His Met Tyr Arg Ser

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25

30

Gln Lys Ala Arg Glu Trp Phe Asn Arg His His Tyr His Ser Pro His

35

40

45

Pro Lys Val Ser Ser Glu Val His Ile Pro Leu Glu Asp Ala Arg Leu

50

55

60

Ala Ile Pro Thr Phe Trp Gly Leu His Thr Gly Glu Arg Asp Trp His

65

70

75

80

Leu Gly Gln Gly Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr

85

90

95

Gln Val Asp Pro Asp Leu Ala Asp Gln Leu Ile His Leu Tyr Tyr Phe

100

105

110

Asp Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly His Arg

115

120

125

Val Ser Pro Arg Cys Glu Tyr Arg Ala Gly His Ser Lys Val Gly Ser

130

135

140

Leu Gln Tyr Leu Ala Ile Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys

145

150

155

160

Pro Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys

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170

175

Pro Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His

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Arg Ile Arg Thr Trp Asn Ser Leu Val Lys Tyr His Met Tyr Arg Ser
 20 25 30

Lys Lys Ala Arg Glu Trp Phe Tyr Arg His His Tyr Gln Ser Pro His
 35 40 45

Pro Lys Val Ser Ser Glu Val His Ile Pro Leu Glu Asp Ala Arg Leu
 50 55 60

Glu Ile Thr Thr Tyr Trp Gly Leu His Thr Gly Glu Arg Asp Trp His
 65 70 75 80

Leu Gly Gln Gly Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr
 85 90 95

His Val Asp Pro Asp Leu Ala Asp His Leu Ile His Leu Cys Tyr Phe
 100 105 110

Asp Cys Leu Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly His Arg
 115 120 125

Val Ser Pro Arg Cys Glu Tyr Arg Ala Gly His Ser Lys Val Gly Ser
 130 135 140

Leu Gln Tyr Leu Ala Ile Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys
 145 150 155 160

Pro Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys
 165 170 175

Pro Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His
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Met Glu Asn Arg Trp Gln Val Met Ile Val Trp Gln Val Asp Arg Met
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Arg Ile Arg Thr Trp Asn Ser Leu Val Lys Tyr His Met Tyr Arg Ser
 20 25 30

Lys Lys Ala Arg Glu Trp Phe Tyr Arg His His Tyr Gln Ser Pro His
 35 40 45

Pro Lys Val Ser Ser Glu Val His Ile Pro Leu Glu Asp Ala Arg Leu
 50 55 60

Val Ile Thr Thr Tyr Trp Gly Leu His Thr Gly Glu Arg Asp Trp His
 65 70 75 80

Leu Gly Gln Gly Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr
 85 90 95

His Val Asp Pro Asp Leu Ala Asp Gln Leu Ile His Leu Tyr Tyr Phe
 100 105 110

Asp Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly His Arg
 115 120 125

Val Ser Pro Arg Cys Glu Tyr Arg Ala Gly His Ser Lys Val Gly Ser
 130 135 140

Leu Gln Tyr Leu Ala Ile Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys
 145 150 155 160

Pro Pro Leu Ala Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys
 165 170 175

Pro Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His
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Arg Ile Arg Thr Trp Asn Ser Leu Val Lys Tyr His Met Tyr Arg Ser
 20 25 30

Lys Lys Ala Arg Glu Trp Phe Tyr Arg His His Tyr Gln Ser Pro His
 35 40 45

Pro Lys Val Ser Ser Glu Val His Ile Pro Leu Glu Asp Ala Arg Leu
 50 55 60

Val Ile Thr Thr Tyr Trp Gly Leu His Thr Gly Glu Arg Asp Trp His
 65 70 75 80

Leu Gly Gln Gly Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr
 85 90 95

Gln Val Asp Pro Asp Leu Ala Asp His Leu Ile His Leu Tyr Tyr Phe
 100 105 110

Asp Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly His Arg
 115 120 125

Val Ser Pro Arg Cys Glu Tyr Arg Ala Gly His Ser Lys Val Gly Ser
 130 135 140

Leu Gln Tyr Leu Ala Ile Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys
 145 150 155 160

Pro Pro Leu Ala Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys
 165 170 175

Pro Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His
 180 185 190

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Arg Ile Arg Thr Trp Asn Ser Leu Val Lys Tyr His Met Tyr Arg Ser
 20 25 30

Lys Lys Ala Arg Glu Trp Phe Tyr Arg His His Tyr Gln Ser Pro His
 35 40 45

Pro Lys Val Ser Ser Glu Val His Ile Pro Leu Glu Asp Ala Arg Leu
 50 55 60

Val Ile Thr Thr Phe Trp Gly Leu His Thr Gly Glu Arg Asp Trp His
 65 70 75 80

Leu Gly Gln Gly Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr
 85 90 95

His Val Asp Pro Asp Leu Ala Asp Gln Leu Ile His Leu Tyr Tyr Phe
 100 105 110

Asp Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly His Arg
 115 120 125

Val Ser Pro Arg Cys Glu Tyr Arg Ala Gly His Ser Lys Val Gly Ser
 130 135 140

Leu Gln Tyr Leu Ala Ile Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys
 145 150 155 160

Pro Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys
 165 170 175

Pro Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His
 180 185 190

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 Met Glu Asn Arg Trp Gln Val Met Ile Val Trp Gln Val Asp Arg Met
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 Arg Ile Arg Thr Trp Asn Ser Leu Val Lys Tyr His Met Tyr Arg Ser
 20 25 30
 Lys Lys Ala Arg Glu Trp Phe Asn Arg His His Tyr His Arg Pro His
 35 40 45
 Pro Lys Val Ser Ser Glu Val His Ile Pro Leu Glu Asp Ala Arg Leu
 50 55 60
 Glu Ile Thr Thr Phe Trp Gly Leu His Thr Gly Glu Arg Asp Trp His
 65 70 75 80
 Leu Gly Gln Gly Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr
 85 90 95
 Gln Val Asp Pro Asp Leu Ala Asp Gln Leu Ile His Leu Tyr Tyr Phe
 100 105 110
 Asp Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly His Arg
 115 120 125
 Val Ser Pro Arg Cys Glu Tyr Arg Ala Gly His Ser Lys Val Gly Ser
 130 135 140
 Leu Gln Tyr Leu Ala Ile Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys
 145 150 155 160
 Pro Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys
 165 170 175
 Pro Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His
 180 185 190

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 1 5 10 15

Arg Ile Arg Thr Trp Asn Ser Leu Val Lys Tyr His Met Tyr Arg Ser
 20 25 30

Gln Lys Glu Arg Glu Trp Phe Asn Arg His His Tyr His Ser Pro His
 35 40 45

Pro Glu Gln Ser Ser Thr Ala His Ile Pro Leu Val Asp Gly Arg Leu
 50 55 60

Glu Lys Ile Ala Val Trp Ser Leu Asp Thr Gly Glu Gly Val Trp His
 65 70 75 80

Arg Gly His Arg Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr
 85 90 95

Gln Val Asp Pro Asp Leu Val Asp Gln Leu Ile His Leu Tyr Tyr Phe
 100 105 110

Asp Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly His Arg
 115 120 125

Val Ser Pro Arg Cys Glu Tyr Arg Ala Gly His Ser Lys Val Gly Ser
 130 135 140

Leu Gln Tyr Leu Ala Ile Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys
 145 150 155 160

Pro Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys
 165 170 175

Pro Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His
 180 185 190

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 Arg Ile Arg Thr Trp Asn Ser Leu Val Lys His His Met Tyr Val Ser
 20 25 30
 Lys Lys Ala Lys Lys Trp Phe Tyr Arg His His Tyr Glu Ser Pro His
 35 40 45
 Pro Lys Val Ser Ser Thr Ala His Ile Pro Leu Gly Asp Gly Arg Leu
 50 55 60
 Glu Lys Thr Ala Val Trp Ser Leu Gln Ala Gly Asp Gly Val Trp His
 65 70 75 80
 Arg Gly His Pro Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr
 85 90 95
 Gln Val Asp Pro Asp Leu Val Asp Gln Leu Ile His Leu Tyr Tyr Phe
 100 105 110
 Asp Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly Tyr Arg
 115 120 125
 Val Ser Pro Arg Cys Glu Tyr Gln Ala Gly His Asn Lys Val Gly Ser
 130 135 140
 Leu Gln Tyr Leu Ala Leu Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys
 145 150 155 160
 Pro Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys
 165 170 175
 Pro Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His
 180 185 190

<210> 15
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 <212> PRT
 <213> Artificial Sequence

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 Arg Ile Arg Ala Trp Asn Ser Leu Val Lys His His Met Tyr Val Ser
 20 25 30
 Lys Lys Ala Arg Thr Trp Phe Ser Arg His His Tyr Gly Ser Pro His
 35 40 45
 Pro Lys Val Cys Ser Glu Val His Ile Pro Leu Gly Asp Ala Arg Leu
 50 55 60
 Val Ile Thr Thr Tyr Trp Ser Leu His Ala Gly Glu Asp Trp His Val
 65 70 75 80
 Gly Gln Arg Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr Gln
 85 90 95
 Val Asp Pro Asp Leu Ala Asp Gln Leu Ile His Leu Tyr Tyr Phe Asp
 100 105 110
 Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly Tyr Arg Val
 115 120 125
 Ser Pro Arg Cys Glu Tyr Gln Ala Gly His Asn Lys Val Gly Ser Leu
 130 135 140
 Gln Tyr Leu Ala Leu Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys Pro
 145 150 155 160
 Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys Pro
 165 170 175
 Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His
 180 185 190

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15

Arg Ile Arg Ala Trp Asn Ser Leu Val Lys His His Thr Tyr Phe Ser

20

25

30

Lys Lys Ala Lys Lys Trp Phe Tyr Arg His His Tyr Glu Ser Pro His

35

40

45

Pro Asn Val Ser Ser Glu Val His Ile Pro Leu Gly Asp Ala Arg Leu

50

55

60

Val Thr Thr Pro Tyr Trp Gly Leu His Gly Gly Glu Arg Asp Trp Tyr

65

70

75

80

Leu Ala Gln Gly Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr

85

90

95

Gln Val Asp Pro Asp Leu Ala Asp Gln Leu Ile His Leu Tyr Tyr Phe

100

105

110

Asp Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly Tyr Arg

115

120

125

Val Ser Pro Arg Cys Glu Tyr Gln Ala Gly His Asn Lys Val Gly Ser

130

135

140

Leu Gln Tyr Leu Ala Leu Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys

145

150

155

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Pro Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys

165

170

175

Pro Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His

180

185

190

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 1 5 10 15

Arg Ile Arg Ala Trp Asn Ser Leu Val Lys His His Met Tyr Val Ser
 20 25 30

Lys Lys Ala Lys Lys Trp Phe Tyr Arg His His Tyr Glu Ser Pro His
 35 40 45

Pro Lys Val Ser Ser Glu Val His Ile Pro Leu Gly Asp Ala Arg Leu
 50 55 60

Val Ile Thr Thr Tyr Trp Gly Leu His Ala Gly Glu Arg Asp Trp His
 65 70 75 80

Leu Gly Gln Gly Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr
 85 90 95

Gln Val Asp Pro Asp Leu Ala Asp Gln Leu Ile His Leu Tyr Tyr Phe
 100 105 110

Asp Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly Tyr Arg
 115 120 125

Val Ser Pro Arg Cys Glu Tyr Gln Ala Gly His Asn Lys Val Gly Ser
 130 135 140

Leu Gln Tyr Leu Ala Leu Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys
 145 150 155 160

Pro Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys
 165 170 175

Pro Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His
 180 185 190

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 Arg Ile Arg Ala Trp Asn Ser Leu Val Lys His His Met Tyr Val Ser
 20 25 30
 Lys Asn Ala Lys Lys Trp Phe Tyr Arg His His Tyr Asp Ser Pro His
 35 40 45
 Pro Val Gln Ser Ser Thr Ala His Ile Pro Leu Gly Asp Gly Arg Leu
 50 55 60
 Gln Lys Ile Ala Phe Trp Ser Leu Asp Ala Gly Glu Arg Asp Trp His
 65 70 75 80
 Leu Gly Gln Gly Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr
 85 90 95
 Gln Val Asp Pro Asp Leu Ala Asp Gln Leu Ile His Leu Tyr Tyr Phe
 100 105 110
 Asp Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly Tyr Arg
 115 120 125
 Val Ser Pro Arg Cys Glu Tyr Gln Ala Gly His Asn Lys Val Gly Ser
 130 135 140
 Leu Gln Tyr Leu Ala Leu Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys
 145 150 155 160
 Pro Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys
 165 170 175
 Pro Gln Lys Thr Lys Gly His Arg Gly Arg His Thr Met Asn Gly His
 180 185 190

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Met Glu Asn Arg Trp Gln Val Met Ile Val Trp Gln Val Asp Arg Met
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Arg Ile Arg Ala Trp Asn Ser Leu Val Lys His His Met Tyr Val Ser
 20 25 30

Lys Lys Ala Lys Lys Trp Phe Tyr Arg His His Tyr Asp Ser Pro His
 35 40 45

Pro Lys Val Ser Ser Glu Val His Ile Pro Leu Gly Asp Ala Arg Leu
 50 55 60

Glu Thr Thr Thr Tyr Trp Gly Leu His Ala Gly Glu Arg Asp Trp His
 65 70 75 80

Leu Gly Gln Gly Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr
 85 90 95

His Val Asp Pro Asp Leu Ala Asp Gln Leu Ile His Leu Tyr Tyr Phe
 100 105 110

Asp Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly Tyr Arg
 115 120 125

Val Ser Pro Arg Cys Glu Tyr Gln Ala Gly His Asn Lys Val Gly Ser
 130 135 140

Leu Gln Tyr Leu Ala Leu Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys
 145 150 155 160

Pro Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys
 165 170 175

Pro Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His
 180 185 190

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1

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10

15

Thr Ile Arg Ala Trp Asn Ser Leu Val Lys His His Met Tyr Val Ser

20

25

30

Lys Lys Ala Lys Lys Trp Phe Tyr Arg His His Tyr Glu Ser Pro His

35

40

45

Pro Lys Val Ser Ser Glu Val His Ile Pro Leu Gly Asp Ala Arg Leu

50

55

60

Val Ile Thr Thr Tyr Trp Gly Leu His Ala Gly Glu Arg Asp Trp His

65

70

75

80

Leu Gly Gln Gly Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr

85

90

95

Gln Val Asp Pro Asp Leu Ala Asp Gln Leu Thr His Leu Tyr Tyr Phe

100

105

110

Asp Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly Tyr Arg

115

120

125

Val Ser Pro Arg Cys Glu Tyr Gln Ala Gly His Asn Lys Val Gly Ser

130

135

140

Leu Gln Tyr Leu Ala Leu Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys

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150

155

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Pro Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys

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Pro Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His

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Met Glu Asn Arg Trp Gln Val Met Ile Val Trp Gln Val Asp Arg Met

1

5

10

15

Arg Ile Arg Ala Trp Asn Ser Leu Val Lys His His Met Tyr Val Ser

20

25

30

Lys Lys Ala Lys Lys Trp Phe Asn Arg His His Tyr Asp Arg Pro His

35

40

45

Pro Lys Val Ser Ser Glu Val His Ile Pro Leu Gly Asp Ala Arg Leu

50

55

60

Glu Ile Thr Thr Phe Trp Gly Leu His Ala Gly Glu Arg Asp Trp His

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75

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Leu Gly Gln Arg Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr

85

90

95

Gln Val Asp Pro Asp Leu Ala Asp Gln Leu Thr His Leu Tyr Tyr Phe

100

105

110

Asp Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly Tyr Arg

115

120

125

Val Ser Pro Arg Cys Glu Tyr Gln Ala Gly His Asn Lys Val Gly Ser

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135

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Leu Gln Tyr Leu Ala Leu Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys

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Pro Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys

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Pro Gln Lys Thr Lys Gly Thr Glu Gly Ala Ile Gln

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185

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 Met Glu Asn Arg Trp Gln Val Met Ile Val Trp Gln Val Asp Arg Met
 1 5 10 15
 Arg Ile Arg Ala Trp Asn Ser Leu Val Lys His His Met Phe Val Ser
 20 25 30
 Lys Lys Ala Lys Lys Trp Phe Tyr Arg His His Tyr Glu Ser Pro His
 35 40 45
 Pro Lys Val Ser Ser Glu Val His Ile Pro Leu Gly Asp Ala Arg Leu
 50 55 60
 Glu Ile Thr Thr Phe Trp Gly Leu His Ala Gly Glu Arg Asp Trp His
 65 70 75 80
 Leu Gly Gln Gly Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr
 85 90 95
 Gln Val Asp Pro Asp Leu Ala Asp Gln Leu Ile His Leu Tyr Tyr Phe
 100 105 110
 Gly Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly Tyr Arg
 115 120 125
 Val Ser Pro Arg Cys Glu Tyr Gln Ala Gly His Asn Lys Val Gly Ser
 130 135 140
 Leu Gln Tyr Leu Gly Leu Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys
 145 150 155 160
 Pro Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys
 165 170 175
 Pro Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His
 180 185 190

<210> 23
 <211> 192
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Novel Sequence

<400> 23
 Met Glu Asn Arg Trp Gln Val Met Ile Val Trp Gln Val Asp Arg Met
 1 5 10 15

Arg Ile Arg Ala Trp Asn Ser Leu Val Lys His His Met Tyr Val Ser
 20 25 30

Lys Lys Ala Lys Lys Trp Phe Tyr Arg His His Tyr Glu Ser Pro His
 35 40 45

Pro Gln Val Ser Ser Glu Val His Ile Pro Leu Gly Asp Ala Arg Leu
 50 55 60

Glu Ile Thr Thr Tyr Trp Gly Leu His Ala Gly Glu Arg Asp Trp His
 65 70 75 80

Leu Gly Gln Gly Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr
 85 90 95

Gln Val Asp Pro Asp Leu Ala Asp Gln Leu Ile His Leu Tyr Tyr Phe
 100 105 110

Asp Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly Tyr Arg
 115 120 125

Val Ser Pro Arg Cys Glu Tyr Gln Ala Gly His Asn Lys Val Gly Ser
 130 135 140

Leu Gln Tyr Leu Ala Leu Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys
 145 150 155 160

Pro Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys
 165 170 175

Pro Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His
 180 185 190

<210> 24
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Novel Sequence

<400> 24
 Ile Glu Trp Arg Lys Lys Arg Tyr
 1 5

<210> 25
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Novel Sequence

<400> 25
 Asp Arg Trp Asn Lys Pro Gln
 1 5

<210> 26
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Novel Sequence

<400> 26
 Ser Leu Gln Tyr Leu Ala
 1 5

<210> 27
 <211> 579
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Novel Sequence

<400> 27

atggaaaaca gatggcaggt gattattgtg tggcaggtag acaggatgag gattagaaca 60
 tgaacacagt tagtaaaata ccatatgtat tgatcaaga aagctaggga atggttttat 120
 tgacatcact atcaaaagtc tcatcaaaa gtaagttcag aagtacacat cccactagag 180
 gatgctagat tggaaataac atcatattgg ggtctgcata caggagaaag agactggcat 240
 ttgggtcagg gagtctccat agaattggagg aaaaggagat atagcacaca cgtcgacct 300
 gatctagcag accaactaat tcatctgtat tatittgatt gtitttcaga atctgctata 360
 agaaaagcca tattaggaca cagagttagt ctaggtgtg aatatcgagc aggcacatagc 420
 aaggttagat cactacagta ctggccaata gcagcattaa taacacaaa aaagataaag 480
 ccacctttgg cgagtgtcag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
 aagggccaca gagggagcca tacaatgaat ggacacatag 579

<210> 28

<211> 579

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 28

atggaaaaca gatggcaggt gatgattgtg tggcaggtag acaggatgag gattagaaca 60
 tgaacacagt tagtaaaata ccatatgtat agatcaaga aagctaggga atggttttat 120
 agacatcact atcaaaagtc tcatcaaga gtaagttcag aagtacacat cccactagag 180
 gatgctagat tggaaataac aacatattgg ggtctgcata caggagaaag agactggcat 240
 ttgggtcagg gagtctccat agaattggagg aaaaggagat atagcacaca agtagacct 300
 gatctagcag accaactaat tcatctgtat tatittgatt gtitttcaga atctgctata 360
 agaaaagcca tattaggaca cagagttagt ctaggtgtg aatatcgagc aggcacatagc 420
 aaggttagat cactacagta ctggccaata gcagcattaa taacacaaa aaagataaag 480
 ccacctttgg cgagtgtcag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
 aagggccaca gagggagcca tacaatgaat ggacacatag 579

<210> 29

<211> 579

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 29

atggaaaaca gatggcaggt gatgattgtg tggcaggtag acaggatgag gattagaaca 60
 tgaacacagt tagtaaaata ccatatgtat agatcaaga aagctaggga atggttttat 120
 agacatcact atcaaaagtc tcatcaaaa gtaagttcag aagtacacat cccactagag 180
 gatgctagat tggaaataac aacatattgg ggtctgcata caggagaaag agactggcat 240
 ttgggtcagg gagtctccat agaattggagg aaaaggagat atagcacaca agtagacct 300

gatctagcag accaactaat tcattctgtat tattttgatt gtttttcaga atctgctata 360
 agaaaagcca tattaggaca cagagttagt cctaggtgtg aatctcgagc aggacatagc 420
 aaggtaggat cactacagta ctgggcaata gcagcattaa taacaccaa aaagataaag 480
 ccacctttgc cgagtgtcag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
 aagggccaca gagggagcca tacaatgaat ggacactag 579

<210> 30

<211> 579

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 30

atggaaaaa gatggcaggt gatgattgtg tggcaggtag acaggatgag gattagaaca 60
 tggaaacagtt tagtaacata ccatatgtat agatcacaga aagctaggga atggtttat 120
 agacatcatc atcacagicc tcattccaaa gtaagttcag aagtcacat cccactagag 180
 gatgctagat tggcaatacc aacattttgg ggtctgcata caggagaaag agactggcat 240
 ttgggtcagg gagtctccat agaattggagg aaaaggagat atagcacaca agtagacct 300
 gatctagcag accaactaat tcattctgtat tattttgatt gtttttcaga atctgctata 360
 agaaaagcca tattaggaca cagagttagt cctaggtgtg aatctcgagc aggacatagc 420
 aaggtaggat cactacagta ctgggcaata gcagcattaa taacaccaa aaagataaag 480
 ccacctttgc cgagtgtcag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
 aagggccaca gagggagcca tacaatgaat ggacactag 579

<210> 31

<211> 579

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 31

atggaaaaa gatggcaggt gatgattgtg tggcaggtag acaggatgag gattagaaca 60
 tggaaacagtt tagtaaaata ccatatgtat agatcaaaga aagctaggga atggtttat 120
 agacatcatc atcaaagtc tcattccaaa gtaagttcag aagtcacat cccactagag 180
 gatgctagat tggaaataac aacattttgg ggtctgcata caggagaaag agactggcat 240
 ttgggtcagg gagtctccat agaattggagg aaaaggagat atagcacaca cgtcgacct 300
 gatctgcag accacctaat tcattctgtt tattttgatt gtcttcaga atctgctata 360
 agaaaagcca tattaggaca cagagttagt cctaggtgtg aatctcgagc aggacatagc 420
 aaggtaggat cactacagta ctgggcaata gcagcattaa taacaccaa aaagataaag 480
 ccacctttgc cgagtgtcag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
 aagggccaca gagggagcca tacaatgaat ggacactag 579

<210> 32
 <211> 579
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Novel Sequence

<400> 32
 atggaaaaca gatggcaggt gatgattgtg tggcaggtag acaggatgag gattagaaca 60
 tggaaacagt tagtaaaata ccatatgtat agatcaaaga aagctaggga atggttttat 120
 agacatcact atcaaagtc tcatccaaaa gtaagttcag aagtacacat cccactagag 180
 gatgctagat tggtaataac aacatattgg ggtctgcata caggagaaag agactggcat 240
 ttgggtcagg gagtctccat agaatggagg aaaaggagat atagcacaca cgtagaccct 300
 gatctagcag accaactaat tcatctgtat tattttgatt gttttcaga atctgctata 360
 agaaaagcca tattaggaca cagagttagt cctaggtgtg aatatcgagc aggacatagc 420
 aaggtaggat cactacagta ctgggcaata gcagcattaa taacacccaa aaagataaag 480
 ccacctttgg cgagtgtcag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
 aagggccaca gagggagcca tacaatgaat ggacactag 579

<210> 33
 <211> 579
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Novel Sequence

<400> 33
 atggaaaaca gatggcaggt gatgattgtg tggcaggtag acaggatgag gattagaaca 60
 tggaaacagt tagtaaaata ccatatgtat agatcaaaga aagctaggga atggttttat 120
 agacatcact atcaaagtc tcatccaaaa gtaagttcag aagtacacat cccactagag 180
 gatgctagat tggtaataac aacatattgg ggtctgcata caggagaaag agactggcat 240
 ttgggtcagg gagtctccat agaatggagg aaaaggagat atagcacaca agtagaccct 300
 gatctagcag accaccta at tcatctgtat tattttgatt gttttcaga atctgctata 360
 agaaaagcca tattaggaca cagagttagt cctaggtgtg aatatcgagc aggacatagc 420
 aaggtaggat cactacagta ctgggcaata gcagcattaa taacacccaa aaagataaag 480
 ccacctttgg cgagtgtcag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
 aagggccaca gagggagcca tacaatgaat ggacactag 579

<210> 34
 <211> 579
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 34

atggaaaaca gatggcaggt gatgattgtg tggcaggtag acaggatgag gattagaaca 60
 tggaaacagt tagtaaaata ccatatgtat agatcaaaga aagctaggga atggtttat 120
 agacatcact atcaaagtc tcatccaaaa gtaagttcag aagtacacat ccactagag 180
 gatgctagat tggtaataac aacattttgg ggtctgcata caggagaaag agactggcat 240
 ttgggtcagg gagtctccat agaattggagg aaaaggagat atagcacaca cgtagacct 300
 gatctagcag accaactaat tcatctgtat tattttgatt gttttcaga atctgctata 360
 agaaaagcca tattaggaca cagagttagt cctaggtgtg aatatcgagc aggacatagc 420
 aaggtaggag cactacagta ctggcaata gcagcattaa taacacaaaa aaagataaag 480
 ccacctttgc cgagtgtcag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
 aagggtcaca gagggagcca tacaatgaat ggacactag 579

<210> 35

<211> 579

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 35

atggaaaaca gatggcaggt gatgattgtg tggcaggtag acaggatgag gattagaaca 60
 tggaaacagt tagtaaaata ccatatgtat agatcaaaga aagctaggga atggtttat 120
 agacatcact atcaccgtcc tcatccaaaa gtaagttcag aagttccat ccactagag 180
 gatgctagat tggaaataac aacattttgg ggtctgcata caggagaaag agactggcat 240
 ttgggtcagg gagtctccat agaattggagg aaaaggagat atagcacaca agtagacct 300
 gatctagcag accaactaat tcatctgtat tattttgatt gttttcaga atctgctata 360
 agaaaagcca tattaggaca cagagttagt cctaggtgtg aatatcgagc aggacatagc 420
 aaggtaggag cactacagta ctggcaata gcagcattaa taacacaaaa aaagataaag 480
 ccacctttgc cgagtgtcag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
 aagggtcaca gagggagcca tacaatgaat ggacactag 579

<210> 36

<211> 584

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 36

atggaaaaca gatggcaggt gatgattgtg tggcaggtag acaggatgag gattagaaca 60

tggaaacagtt tagtaaaata ccatatgtat tgatcaaaaga aaagaaagaa aggggaatggt 120
 ttatagaca tcacatcac agccctcatc cagaacaaag ticaacagcc cacatccgc 180
 tagtggatgg tagattggaa aaaatagcag ttggagtgct ggatacagga gatggcgctc 240
 ggacacaggg gcatcgagtc tccatagaat ggagggaag gagatatagc acacaagtag 300
 accctgatct agtagacca ctaaticatc tgtattattt ttattgtttt tcagaaictg 360
 ctataagaaa agccatatta ggacacagag ttatgcctag gtgtgaatat cgagcaggac 420
 atagcaaggt aggatcacta cagtacttgg caatagcagc attaataaca ccaaaaaaga 480
 taaagccacc ttggccgagt gtcaggaaac tgacagagga tagatgggaac aagccccaga 540
 agaccaaggg ccacagaggg agccatacaa tgaatggaca ctac 584

<210> 37

<211> 579

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 37

atggaaaaa gatggcaggt gatgattgtg tggcaagtag acaggatgag gattagaaca 60
 tggaaacagtt tagtaaaaca ccatatgtat gtttcaaga aagctaagaa atggttttt 120
 agacatcact atgaaagccc tcatccaaaa gtaagtcca cagccacat cccgctagg 180
 gatgtagat tggagaaaa agcagtttgg agtctgcagg caggagatgg agtctggcac 240
 agggggcagc cagtctccat agaatggagg aaaaggagat atagcacaca agtagaccct 300
 gatttggtag accaactaat tcatctgtat tattttgatt gtttttcaga atctgtata 360
 agaaaagcca tattaggata tagagttagt cctaggtgtg aataccaagc aggcataat 420
 aaggtaggat cctacagta ctggcacta gcagcattaa taacccaaa gaagataaag 480
 ccacctttgc ctagtgttag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
 aagggccaca gagggagcca tacaatgaat ggacactag 579

<210> 38

<211> 579

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 38

atggaaaaa gatggcaggt gatgattgtg tggcaagtag acaggatgag gattagagca 60
 tggaaacagtt tagtaaaaca ccatatgtat gtttcaaga aagctaggac atggttttt 120
 agacatcact atgaaagccc tcatccaaaa gtagtttcag aagtacacat cccactagg 180
 gatgctagat tgggtgataa aacatattgg agtctgcagc caggagaatg agactggcat 240
 ttgggtcaga gagtctccat agaatggagg aaaaggagat atagcacaca agtagaccct 300
 gacttggcag accaactaat tcatctgtat tattttgatt gtttttcaga atctgtata 360

agaaaaacca tattaggata tagagttagt cctagggtgtg aataccaagc aggacataat 420
 aaggtaggat ctctacagta ctggcacta gcagcattaa taacacaaa gaagataaag 480
 ccacctttgc ctagtgtgag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
 aagggccaca gaggagacca tacaatgaat ggacactag 579

<210> 39

<211> 579

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 39

atgaaaaaca gatggcaggt gatgattgtg tggcaagtag acaggatgag gattagagca 60
 tggaaacagtt tagtaaaaca ccatatttat ttttcaaaga aagctaagaa atggttttat 120
 agacatcact atgaaagccc tcatccaaac gtaagttcag aagtacacat cccactaggg 180
 gatgctagat tggtgacaac accatattgg ggtctgcatg gaggagaaag agactggtat 240
 ctggctcagg gagtctccat agaattggagg aaaaggagat atagcacaca agtagaccct 300
 gacctggcag accaactaat tcatctgtat tattttgatt gttttcaga atctgctata 360
 agaaaagcca tattaggata tagagttagt cctagggtgtg aataccaagc aggacataat 420
 aaggtaggat ctctacagta ctggcacta gcagcattaa taacacaaa gaagataaag 480
 ccacctttgc ctagtgtgag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
 aagggccaca gaggagacca tacaatgaat ggacactag 579

<210> 40

<211> 579

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 40

atgaaaaaca gatgggaggt gatgattgtg tgggaagtag acaggatgag gattagagca 60
 tggaaacagtt tagtaaaaca ccatatgtat gtttcaaaga aagctaagaa atggttttat 120
 agacatcact atgaaagccc tcatccaaa gtaagttcag aagtacacat cccactaggg 180
 gatgctagat tggtgataac aacatattgg ggtctgcatg caggagaaag agactggcat 240
 ttggctcagg gagtctccat agaattggagg aaaaggagat atagcacaca agtagaccct 300
 gacctggcag accaactaat tcatctgtat tattttgatt gttttcaga atctgctata 360
 agaaaagcca tattaggata tagagttagt cctagggtgtg aataccaagc aggacataat 420
 aaggtaggat ctctacagta ctggcacta gcagcattaa taacacaaa gaagataaag 480
 ccacctttgc ctagtgtgag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
 aagggccaca gaggagacca tacaatgaat ggacactag 579

<210> 41
 <211> 579
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Novel Sequence

<400> 41
 atggaaaaca gatggcaggt gatgattgtg tggcaagtag acaggatgag gattagagca 60
 tggaaacagt tagtaaaaca ccatatgtat gtttcaaaga acgctaagaa atggttttat 120
 cgacatcact atgacagccc tcatccagtc caaagttaa cagcccacat cccgctaggg 180
 gatgttagat tgcagaaaat agcattttgg agtctggatg caggagaaag agactggcat 240
 ttgggtcagg gagtctccat agaattggagg aaaaggagat atagcacaca agtagaccct 300
 gacctggcag accaactaat tcatctgtat tatittgatt gttttcaga atctgctata 360
 agaaaagcca tattaggata tagagttagt cctaggtgtg aataccaagc aggacataat 420
 aaggtaggat ctctacagta ctggcacta gcagcattaa taacaccaa gaagataaag 480
 ccacctttgc ctagtgtgag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
 aaggggcaca gaggggagca tacaatgaat ggacactag 579

<210> 42
 <211> 579
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Novel Sequence

<400> 42
 atggaaaaca gatggcaggt gatgattgtg tggcaagtag acaggatgag gattagagca 60
 tggaaacagt tagtaaaaca ccatatgtat gtttcaaaga aagctaagaa atggttttat 120
 agacatcact atgacagccc tcatccaaaa gtaagttcag aagtacacat cccactaggg 180
 gatgctagat tggagataac aacatattgg ggtctgcatg caggagaaag agactggcat 240
 ttgggtcagg gagtctccat agaattggagg aaaaggagat atagcacaca cgtagaccct 300
 gacctggcag accaactaat tcatctgtat tatittgatt gttttcaga atctgctata 360
 agaaaagcca tattaggata tagagttagt cctaggtgtg aataccaagc aggacataat 420
 aaggtaggat ctctacagta ctggcacta gcagcattaa taacaccaa gaagataaag 480
 ccacctttgc ctagtgtgag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
 aaggggcaca gaggggagcca tacaatgaat ggacactag 579

<210> 43
 <211> 579
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 43

atggaaaaa gatggcaggt gatgattgtg tggcaagtag acaggatgac gattagagca 60
 tggaacagtt tagtaaaaca ccatatgtat gttcaaaaga aagctaagaa atggttttat 120
 agacatacct atgaaagccc tcatccaaaa gtaagtccag aagtacacat ccactaggg 180
 gatgctagat tggtgataac aacatatggg ggtctgcatg caggagaaag agactggcat 240
 ttgggtcagg gagtctccat agaattggagg aaaaggagat atagcacaca agtagacct 300
 gacttggcag accaactaac tcatctgtat tattttgatt gttttcaga atctgctata 360
 agaaaagcca tattaggata tagagttagt cctaggtgtg aataccaagc aggacataat 420
 aaggtaggat ctctacagta ctggcacta gcagcattaa taacaccaa gaagataaag 480
 ccaccttgc ctagtgtgag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
 aagggcaca gagggagcca tacaatgaat ggacactag 579

<210> 44

<211> 578

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 44

atggaaaaa gatggcaggt gatgattgtg tggcaagtag acaggatgag gattagagca 60
 tggaacagtt tagtaaaaca ccatatgtat gttcaaaaga aagctaagaa atggtttaat 120
 agacatcact atgaccgccc tcatccaaaa gtaagtccag aagtccacat ccactaggg 180
 gatgctagat tggagataac aacattttgg ggtctgcatg caggagaaag agactggcat 240
 ttgggtcagc gagtctccat agaattggagg aaaaggagat atagcacaca agtagacct 300
 gacttggcag accaactaac tcatctgtat tattttgatt gttttcaga atctgctata 360
 agaaaagcca tattaggata tagagttagt cctaggtgtg aataccaagc aggacataat 420
 aaggtaggat ctctacagta ctggcacta gcagcattaa taacaccaa gaagataaag 480
 ccaccttgc ctagtgtgag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
 aagggcacag agggagccat acaatgaatg gacactag 578

<210> 45

<211> 579

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 45

atggaaaaa gatggcaggt gatgattgtg tggcaagtag acaggatgag gattagagca 60

tggaaacagtt tagtaaaaca ccatatgttt gtttcaaaga aagctaagaa atggttttat 120
 agacatcact atgaaagccc tcattccaaa gtaagttcag aagtacacat cccactaggg 180
 gatgctagat tggagataac aacattttgg ggtctgcatg caggagaaag agactggcat 240
 ttgggtcagg gagtctccat agaattggagg aaaaggagat atagcacaca agtagaccct 300
 gacctggcag accaactaat tcattctgtat tattttggtt gtttttcaga atctgctata 360
 agaaaagcca tattaggata tagagttagt cctaggtgtg aataccaagc aggacataat 420
 aaggtaggat ctctacagta ctgggcacta gcagcattaa taacacaaa gaagataaag 480
 ccacctttgc ctagtgtgag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
 aaggggccaca gaggggagcca tacaatgaat ggacactag 579

<210> 46

<211> 579

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 46

atggaaaaca gatggcaggt gatgattgtg tggcaagtag acaggatgag gattagagca 60
 tggaaacagtt tagtaaaaca ccatatgtat gtttcaaaga aagctaagaa atggttttat 120
 agacatcact atgaaagccc tcattccaaa gtaagttcag aagtacacat cccactaggg 180
 gatgctagat tggagataac aacattttgg ggtctgcatg caggagaaag agactggcat 240
 ttgggtcagg gagtctccat agaattggagg aaaaggagat atagcacaca agtagaccct 300
 gacctggcag accaactaat tcattctgtat tattttgatt gtttttcaga atctgctata 360
 agaaaagcca tattaggata tagagttagt cctaggtgtg aataccaagc aggacataat 420
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 ccacctttgc ctagtgtgag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
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<110> Ayyavoo, Velpandi
Nagashunmugam, Thandavarayan
Weiner, David B.
University of Pennsylvania

<120> ATTENUATED VIF DNA IMMUNIZATION CASSETTES FOR GENETIC
VACCINES

<130> UPAP-0263

<140> HEREWITH

<141> 1998-09-18

<160> 46

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1 5 10 15

Arg Ile Arg Thr Trp Asn Ser Leu Val Lys His His Met Tyr Val Ser
20 25 30

Lys Lys Ala Arg Trp Phe Tyr Arg His His Tyr Glu Ser Pro His Pro
35 40 45

Lys Val Ser Ser Glu Val His Ile Pro Leu Gly Asp Ala Arg Leu Glu
50 55 60

Thr Thr Thr Tyr Trp Gly Leu His Gly Glu Arg Asp Trp His Leu Gly
65 70 75 80

Gln Gly Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr Gln Val
85 90 95

Asp Pro Asp Leu Ala Asp Gln Leu Ile His Leu Tyr Tyr Phe Asp Cys
100 105 110

Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly Tyr Arg Val Ser
115 120 125

Pro Arg Cys Glu Tyr Gln Ala Gly His Asn Lys Val Gly Ser Leu Gln
130 135 140

Tyr Leu Ala Leu Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys Pro Pro
145 150 155 160

Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys Pro Gln
165 170 175

Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His
180 185 190

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<210> 4

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<223> Description of Artificial Sequence: Novel Sequence

<400> 4

Met Glu Asn Arg Trp Gln Val Ile Ile Val Trp Gln Val Asp Arg Met
1 5 10 15

Arg Ile Arg Thr Trp Asn Ser Leu Val Lys Tyr His Met Tyr Ser Lys
20 25 30

Lys Ala Arg Glu Trp Phe Tyr His His Tyr Gln Ser Pro His Pro Lys
35 40 45

Val Ser Ser Glu Val His Ile Pro Leu Glu Asp Ala Arg Leu Glu Ile
50 55 60

Thr Ser Phe Trp Gly Leu His Thr Gly Glu Arg Asp Trp His Leu Gly
65 70 75 80

Gln Gly Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr His Val
85 90 95

Asp Pro Asp Leu Ala Asp Gln Leu Ile His Leu Tyr Tyr Phe Asp Cys
100 105 110

Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly His Arg Val Ser
115 120 125

Pro Arg Cys Glu Tyr Arg Ala Gly His Ser Lys Val Gly Ser Leu Gln
130 135 140

Tyr Leu Ala Ile Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys Pro Pro
145 150 155 160

Leu Ala Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys Pro Gln
165 170 175

Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His
180 185 190

<210> 5

<211> 192

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<223> Description of Artificial Sequence: Novel Sequence

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Met Glu Asn Arg Trp Gln Val Met Ile Val Trp Gln Val Asp Arg Met

1 5 10 15

Arg Ile Arg Thr Trp Asn Ser Leu Val Lys Tyr His Met Tyr Arg Ser

20 25 30

Lys Lys Ala Arg Glu Trp Phe Tyr Arg His His Tyr Gln Ser Pro His

35 40 45

Pro Arg Val Ser Ser Glu Val His Ile Pro Leu Glu Asp Ala Arg Leu

50 55 60

Glu Ile Thr Thr Tyr Trp Gly Leu His Thr Gly Glu Arg Asp Trp His

65 70 75 80

Leu Gly Gln Gly Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr

85 90 95

Gln Val Asp Pro Asp Leu Ala Asp Gln Leu Ile His Leu Tyr Tyr Phe

100 105 110

Asp Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly His Arg

115 120 125

Val Ser Pro Arg Cys Glu Tyr Arg Ala Gly His Ser Lys Val Gly Ser

130 135 140

Leu Gln Tyr Leu Ala Ile Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys

145 150 155 160

Pro Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys

165 170 175

Pro Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His

180 185 190

<210> 6

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<223> Description of Artificial Sequence: Novel Sequence

<400> 6

Met Glu Asn Arg Trp Gln Val Met Ile Val Trp Gln Val Asp Arg Met

1

5

10

15

Arg Ile Arg Thr Trp Asn Ser Leu Val Lys Tyr His Met Tyr Arg Ser

20

25

30

Lys Lys Ala Arg Glu Trp Phe Tyr Arg His His Tyr Gln Ser Pro His

35

40

45

Pro Lys Val Ser Ser Glu Val His Ile Pro Leu Glu Asp Ala Arg Leu

50

55

60

Glu Thr Thr Thr Tyr Trp Gly Leu His Thr Gly Glu Arg Asp Trp His

65

70

75

80

Leu Gly Gln Gly Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr

85

90

95

Gln Val Asp Pro Asp Leu Ala Asp Gln Leu Ile His Leu Tyr Tyr Phe

100

105

110

Asp Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly His Arg

115

120

125

Val Ser Pro Arg Cys Glu Tyr Arg Ala Gly His Ser Lys Val Gly Ser

130

135

140

Leu Gln Tyr Leu Ala Ile Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys

145

150

155

160

Pro Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys

165

170

175

Pro Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His

180

185

190

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<223> Description of Artificial Sequence: Novel Sequence

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Met Glu Asn Arg Trp Gln Val Met Ile Val Trp Gln Val Asp Arg Met

1

5

10

15

Arg Ile Arg Thr Trp Asn Ser Leu Val Thr Tyr His Met Tyr Arg Ser

20

25

30

Gln Lys Ala Arg Glu Trp Phe Asn Arg His His Tyr His Ser Pro His

35

40

45

Pro Lys Val Ser Ser Glu Val His Ile Pro Leu Glu Asp Ala Arg Leu

50

55

60

Ala Ile Pro Thr Phe Trp Gly Leu His Thr Gly Glu Arg Asp Trp His

65

70

75

80

Leu Gly Gln Gly Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr

85

90

95

Gln Val Asp Pro Asp Leu Ala Asp Gln Leu Ile His Leu Tyr Tyr Phe

100

105

110

Asp Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly His Arg

115

120

125

Val Ser Pro Arg Cys Glu Tyr Arg Ala Gly His Ser Lys Val Gly Ser

130

135

140

Leu Gln Tyr Leu Ala Ile Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys

145

150

155

160

Pro Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys

165

170

175

Pro Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His

180

185

190

<210> 8

<211> 192

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 8

Met Glu Asn Arg Trp Gln Val Met Ile Val Trp Gln Val Asp Arg Met

1

5

10

15

Arg Ile Arg Thr Trp Asn Ser Leu Val Lys Tyr His Met Tyr Arg Ser

20

25

30

Lys Lys Ala Arg Glu Trp Phe Tyr Arg His His Tyr Gln Ser Pro His

35

40

45

Pro Lys Val Ser Ser Glu Val His Ile Pro Leu Glu Asp Ala Arg Leu

50

55

60

Glu Ile Thr Thr Tyr Trp Gly Leu His Thr Gly Glu Arg Asp Trp His

65

70

75

80

Leu Gly Gln Gly Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr

85

90

95

His Val Asp Pro Asp Leu Ala Asp His Leu Ile His Leu Cys Tyr Phe

100

105

110

Asp Cys Leu Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly His Arg

115

120

125

Val Ser Pro Arg Cys Glu Tyr Arg Ala Gly His Ser Lys Val Gly Ser

130

135

140

Leu Gln Tyr Leu Ala Ile Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys

145

150

155

160

Pro Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys

165

170

175

Pro Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His

180

185

190

<210> 9

<211> 192

<212> PRT

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<223> Description of Artificial Sequence: Novel Sequence

<400> 9

Met Glu Asn Arg Trp Gln Val Met Ile Val Trp Gln Val Asp Arg Met

1 5 10 15

Arg Ile Arg Thr Trp Asn Ser Leu Val Lys Tyr His Met Tyr Arg Ser

20 25 30

Lys Lys Ala Arg Glu Trp Phe Tyr Arg His His Tyr Gln Ser Pro His

35 40 45

Pro Lys Val Ser Ser Glu Val His Ile Pro Leu Glu Asp Ala Arg Leu

50 55 60

Val Ile Thr Thr Tyr Trp Gly Leu His Thr Gly Glu Arg Asp Trp His

65 70 75 80

Leu Gly Gln Gly Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr

85 90 95

His Val Asp Pro Asp Leu Ala Asp Gln Leu Ile His Leu Tyr Tyr Phe

100 105 110

Asp Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly His Arg

115 120 125

Val Ser Pro Arg Cys Glu Tyr Arg Ala Gly His Ser Lys Val Gly Ser

130 135 140

Leu Gln Tyr Leu Ala Ile Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys

145 150 155 160

Pro Pro Leu Ala Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys

165 170 175

Pro Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His

180 185 190

<210> 10

<211> 192

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 10

Met Glu Asn Arg Trp Gln Val Met Ile Val Trp Gln Val Asp Arg Met

1 5 10 15

Arg Ile Arg Thr Trp Asn Ser Leu Val Lys Tyr His Met Tyr Arg Ser

20 25 30

Lys Lys Ala Arg Glu Trp Phe Tyr Arg His His Tyr Gln Ser Pro His

35 40 45

Pro Lys Val Ser Ser Glu Val His Ile Pro Leu Glu Asp Ala Arg Leu

50 55 60

Val Ile Thr Thr Tyr Trp Gly Leu His Thr Gly Glu Arg Asp Trp His

65 70 75 80

Leu Gly Gln Gly Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr

85 90 95

Gln Val Asp Pro Asp Leu Ala Asp His Leu Ile His Leu Tyr Tyr Phe

100 105 110

Asp Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly His Arg

115 120 125

Val Ser Pro Arg Cys Glu Tyr Arg Ala Gly His Ser Lys Val Gly Ser

130 135 140

Leu Gln Tyr Leu Ala Ile Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys

145 150 155 160

Pro Pro Leu Ala Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys

165 170 175

Pro Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His

180 185 190

<210> 11

<211> 192

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 11

Met Glu Asn Arg Trp Gln Val Met Ile Val Trp Gln Val Asp Arg Met

1

5

10

15

Arg Ile Arg Thr Trp Asn Ser Leu Val Lys Tyr His Met Tyr Arg Ser

20

25

30

Lys Lys Ala Arg Glu Trp Phe Tyr Arg His His Tyr Gln Ser Pro His

35

40

45

Pro Lys Val Ser Ser Glu Val His Ile Pro Leu Glu Asp Ala Arg Leu

50

55

60

Val Ile Thr Thr Phe Trp Gly Leu His Thr Gly Glu Arg Asp Trp His

65

70

75

80

Leu Gly Gln Gly Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr

85

90

95

His Val Asp Pro Asp Leu Ala Asp Gln Leu Ile His Leu Tyr Tyr Phe

100

105

110

Asp Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly His Arg

115

120

125

Val Ser Pro Arg Cys Glu Tyr Arg Ala Gly His Ser Lys Val Gly Ser

130

135

140

Leu Gln Tyr Leu Ala Ile Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys

145

150

155

160

Pro Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys

165

170

175

Pro Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His

180

185

190

<210> 12

<211> 192

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 12

Met Glu Asn Arg Trp Gln Val Met Ile Val Trp Gln Val Asp Arg Met

1

5

10

15

Arg Ile Arg Thr Trp Asn Ser Leu Val Lys Tyr His Met Tyr Arg Ser

20

25

30

Lys Lys Ala Arg Glu Trp Phe Asn Arg His His Tyr His Arg Pro His

35

40

45

Pro Lys Val Ser Ser Glu Val His Ile Pro Leu Glu Asp Ala Arg Leu

50

55

60

Glu Ile Thr Thr Phe Trp Gly Leu His Thr Gly Glu Arg Asp Trp His

65

70

75

80

Leu Gly Gln Gly Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr

85

90

95

Gln Val Asp Pro Asp Leu Ala Asp Gln Leu Ile His Leu Tyr Tyr Phe

100

105

110

Asp Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly His Arg

115

120

125

Val Ser Pro Arg Cys Glu Tyr Arg Ala Gly His Ser Lys Val Gly Ser

130

135

140

Leu Gln Tyr Leu Ala Ile Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys

145

150

155

160

Pro Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys

165

170

175

Pro Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His

180

185

190

<210> 13

<211> 192

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 13

Met Glu Asn Arg Trp Gln Val Met Ile Val Trp Gln Val Asp Arg Met

1

5

10

15

Arg Ile Arg Thr Trp Asn Ser Leu Val Lys Tyr His Met Tyr Arg Ser

20

25

30

Gln Lys Glu Arg Glu Trp Phe Asn Arg His His Tyr His Ser Pro His

35

40

45

Pro Glu Gln Ser Ser Thr Ala His Ile Pro Leu Val Asp Gly Arg Leu

50

55

60

Glu Lys Ile Ala Val Trp Ser Leu Asp Thr Gly Glu Gly Val Trp His

65

70

75

80

Arg Gly His Arg Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr

85

90

95

Gln Val Asp Pro Asp Leu Val Asp Gln Leu Ile His Leu Tyr Tyr Phe

100

105

110

Asp Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly His Arg

115

120

125

Val Ser Pro Arg Cys Glu Tyr Arg Ala Gly His Ser Lys Val Gly Ser

130

135

140

Leu Gln Tyr Leu Ala Ile Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys

145

150

155

160

Pro Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys

165

170

175

Pro Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His

180

185

190

<210> 14

<211> 192

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 14

Met Glu Asn Arg Trp Gln Val Met Ile Val Trp Gln Val Asp Arg Met

1

5

10

15

Arg Ile Arg Thr Trp Asn Ser Leu Val Lys His His Met Tyr Val Ser

20

25

30

Lys Lys Ala Lys Lys Trp Phe Tyr Arg His His Tyr Glu Ser Pro His

35

40

45

Pro Lys Val Ser Ser Thr Ala His Ile Pro Leu Gly Asp Gly Arg Leu

50

55

60

Glu Lys Thr Ala Val Trp Ser Leu Gln Ala Gly Asp Gly Val Trp His

65

70

75

80

Arg Gly His Pro Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr

85

90

95

Gln Val Asp Pro Asp Leu Val Asp Gln Leu Ile His Leu Tyr Tyr Phe

100

105

110

Asp Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly Tyr Arg

115

120

125

Val Ser Pro Arg Cys Glu Tyr Gln Ala Gly His Asn Lys Val Gly Ser

130

135

140

Leu Gln Tyr Leu Ala Leu Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys

145

150

155

160

Pro Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys

165

170

175

Pro Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His

180

185

190

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<223> Description of Artificial Sequence: Novel Sequence

<400> 15

Met Glu Asn Arg Trp Gln Val Met Ile Val Trp Gln Val Asp Arg Met

1 5 10 15

Arg Ile Arg Ala Trp Asn Ser Leu Val Lys His His Met Tyr Val Ser

20 25 30

Lys Lys Ala Arg Thr Trp Phe Ser Arg His His Tyr Gly Ser Pro His

35 40 45

Pro Lys Val Cys Ser Glu Val His Ile Pro Leu Gly Asp Ala Arg Leu

50 55 60

Val Ile Thr Thr Tyr Trp Ser Leu His Ala Gly Glu Asp Trp His Val

65 70 75 80

Gly Gln Arg Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr Gln

85 90 95

Val Asp Pro Asp Leu Ala Asp Gln Leu Ile His Leu Tyr Tyr Phe Asp

100 105 110

Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly Tyr Arg Val

115 120 125

Ser Pro Arg Cys Glu Tyr Gln Ala Gly His Asn Lys Val Gly Ser Leu

130 135 140

Gln Tyr Leu Ala Leu Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys Pro

145 150 155 160

Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys Pro

165 170 175

Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His

180 185 190

<210> 16

<211> 192

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Novel Sequence

<400> 16

Met Glu Asn Arg Trp Gln Val Met Ile Val Trp Gln Val Asp Arg Met

1 5 10 15

Arg Ile Arg Ala Trp Asn Ser Leu Val Lys His His Thr Tyr Phe Ser

20 25 30

Lys Lys Ala Lys Lys Trp Phe Tyr Arg His His Tyr Glu Ser Pro His

35 40 45

Pro Asn Val Ser Ser Glu Val His Ile Pro Leu Gly Asp Ala Arg Leu

50 55 60

Val Thr Thr Pro Tyr Trp Gly Leu His Gly Gly Glu Arg Asp Trp Tyr

65 70 75 80

Leu Ala Gln Gly Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr

85 90 95

Gln Val Asp Pro Asp Leu Ala Asp Gln Leu Ile His Leu Tyr Tyr Phe

100 105 110

Asp Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly Tyr Arg

115 120 125

Val Ser Pro Arg Cys Glu Tyr Gln Ala Gly His Asn Lys Val Gly Ser

130 135 140

Leu Gln Tyr Leu Ala Leu Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys

145 150 155 160

Pro Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys

165 170 175

Pro Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His

180 185 190

<210> 17

<211> 192

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 17

Met Glu Asn Arg Trp Glu Val Met Ile Val Trp Glu Val Asp Arg Met

1 5 10 15

Arg Ile Arg Ala Trp Asn Ser Leu Val Lys His His Met Tyr Val Ser

20 25 30

Lys Lys Ala Lys Lys Trp Phe Tyr Arg His His Tyr Glu Ser Pro His

35 40 45

Pro Lys Val Ser Ser Glu Val His Ile Pro Leu Gly Asp Ala Arg Leu

50 55 60

Val Ile Thr Thr Tyr Trp Gly Leu His Ala Gly Glu Arg Asp Trp His

65 70 75 80

Leu Gly Gln Gly Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr

85 90 95

Gln Val Asp Pro Asp Leu Ala Asp Gln Leu Ile His Leu Tyr Tyr Phe

100 105 110

Asp Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly Tyr Arg

115 120 125

Val Ser Pro Arg Cys Glu Tyr Gln Ala Gly His Asn Lys Val Gly Ser

130 135 140

Leu Gln Tyr Leu Ala Leu Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys

145 150 155 160

Pro Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys

165 170 175

Pro Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His

180 185 190

<210> 18

<211> 192

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Novel Sequence

<400> 17

Met Glu Asn Arg Trp Gln Val Met Ile Val Trp Gln Val Asp Arg Met

1 5 10 15

Arg Ile Arg Ala Trp Asn Ser Leu Val Lys His His Met Tyr Val Ser

20 25 30

Lys Asn Ala Lys Lys Trp Phe Tyr Arg His His Tyr Asp Ser Pro His

35 40 45

Pro Val Gln Ser Ser Thr Ala His Ile Pro Leu Gly Asp Gly Arg Leu

50 55 60

Gln Lys Ile Ala Phe Trp Ser Leu Asp Ala Gly Glu Arg Asp Trp His

65 70 75 80

Leu Gly Gln Gly Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr

85 90 95

Gln Val Asp Pro Asp Leu Ala Asp Gln Leu Ile His Leu Tyr Tyr Phe

100 105 110

Asp Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly Tyr Arg

115 120 125

Val Ser Pro Arg Cys Glu Tyr Gln Ala Gly His Asn Lys Val Gly Ser

130 135 140

Leu Gln Tyr Leu Ala Leu Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys

145 150 155 160

Pro Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys

165 170 175

Pro Gln Lys Thr Lys Gly His Arg Gly Arg His Thr Met Asn Gly His

180 185 190

<210> 19

<211> 192

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Novel Sequence

<400> 19

Met Glu Asn Arg Trp Gln Val Met Ile Val Trp Gln Val Asp Arg Met

1 5 10 15

Arg Ile Arg Ala Trp Asn Ser Leu Val Lys His His Met Tyr Val Ser

20 25 30

Lys Lys Ala Lys Lys Trp Phe Tyr Arg His His Tyr Asp Ser Pro His

35 40 45

Pro Lys Val Ser Ser Glu Val His Ile Pro Leu Gly Asp Ala Arg Leu

50 55 60

Glu Thr Thr Thr Tyr Trp Gly Leu His Ala Gly Glu Arg Asp Trp His

65 70 75 80

Leu Gly Gln Gly Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr

85 90 95

His Val Asp Pro Asp Leu Ala Asp Gln Leu Ile His Leu Tyr Tyr Phe

100 105 110

Asp Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly Tyr Arg

115 120 125

Val Ser Pro Arg Cys Glu Tyr Gln Ala Gly His Asn Lys Val Gly Ser

130 135 140

Leu Gln Tyr Leu Ala Leu Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys

145 150 155 160

Pro Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys

165 170 175

Pro Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His

180 185 190

<210> 20

<211> 192

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 20

Met Glu Asn Arg Trp Gln Val Met Ile Val Trp Gln Val Asp Arg Met

1 5 10 15

Thr Ile Arg Ala Trp Asn Ser Leu Val Lys His His Met Tyr Val Ser

20 25 30

Lys Lys Ala Lys Lys Trp Phe Tyr Arg His His Tyr Glu Ser Pro His

35 40 45

Pro Lys Val Ser Ser Glu Val His Ile Pro Leu Gly Asp Ala Arg Leu

50 55 60

Val Ile Thr Thr Tyr Trp Gly Leu His Ala Gly Glu Arg Asp Trp His

65 70 75 80

Leu Gly Gln Gly Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr

85 90 95

Gln Val Asp Pro Asp Leu Ala Asp Gln Leu Thr His Leu Tyr Tyr Phe

100 105 110

Asp Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly Tyr Arg

115 120 125

Val Ser Pro Arg Cys Glu Tyr Gln Ala Gly His Asn Lys Val Gly Ser

130 135 140

Leu Gln Tyr Leu Ala Leu Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys

145 150 155 160

Pro Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys

165 170 175

Pro Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His

180 185 190

<210> 21
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<400> 21
Met Glu Asn Arg Trp Gln Val Met Ile Val Trp Gln Val Asp Arg Met
1 5 10 15

Arg Ile Arg Ala Trp Asn Ser Leu Val Lys His His Met Tyr Val Ser
20 25 30

Lys Lys Ala Lys Lys Trp Phe Asn Arg His His Tyr Asp Arg Pro His
35 40 45

Pro Lys Val Ser Ser Glu Val His Ile Pro Leu Gly Asp Ala Arg Leu
50 55 60

Glu Ile Thr Thr Phe Trp Gly Leu His Ala Gly Glu Arg Asp Trp His
65 70 75 80

Leu Gly Gln Arg Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr
85 90 95

Gln Val Asp Pro Asp Leu Ala Asp Gln Leu Thr His Leu Tyr Tyr Phe
100 105 110

Asp Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly Tyr Arg
115 120 125

Val Ser Pro Arg Cys Glu Tyr Gln Ala Gly His Asn Lys Val Gly Ser
130 135 140

Leu Gln Tyr Leu Ala Leu Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys
145 150 155 160

Pro Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys
165 170 175

Pro Gln Lys Thr Lys Gly Thr Glu Gly Ala Ile Gln
180 185

<210> 22

<211> 192

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 22

Met Glu Asn Arg Trp Gln Val Met Ile Val Trp Gln Val Asp Arg Met

1 5 10 15

Arg Ile Arg Ala Trp Asn Ser Leu Val Lys His His Met Phe Val Ser

20 25 30

Lys Lys Ala Lys Lys Trp Phe Tyr Arg His His Tyr Glu Ser Pro His

35 40 45

Pro Lys Val Ser Ser Glu Val His Ile Pro Leu Gly Asp Ala Arg Leu

50 55 60

Glu Ile Thr Thr Phe Trp Gly Leu His Ala Gly Glu Arg Asp Trp His

65 70 75 80

Leu Gly Gln Gly Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr

85 90 95

Gln Val Asp Pro Asp Leu Ala Asp Gln Leu Ile His Leu Tyr Tyr Phe

100 105 110

Gly Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly Tyr Arg

115 120 125

Val Ser Pro Arg Cys Glu Tyr Gln Ala Gly His Asn Lys Val Gly Ser

130 135 140

Leu Gln Tyr Leu Gly Leu Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys

145 150 155 160

Pro Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys

165 170 175

Pro Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His

180 185 190

<210> 23

<211> 192

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 23

Met Glu Asn Arg Trp Gln Val Met Ile Val Trp Gln Val Asp Arg Met

1 5 10 15

Arg Ile Arg Ala Trp Asn Ser Leu Val Lys His His Met Tyr Val Ser

20 25 30

Lys Lys Ala Lys Lys Trp Phe Tyr Arg His His Tyr Glu Ser Pro His

35 40 45

Pro Gln Val Ser Ser Glu Val His Ile Pro Leu Gly Asp Ala Arg Leu

50 55 60

Glu Ile Thr Thr Tyr Trp Gly Leu His Ala Gly Glu Arg Asp Trp His

65 70 75 80

Leu Gly Gln Gly Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr

85 90 95

Gln Val Asp Pro Asp Leu Ala Asp Gln Leu Ile His Leu Tyr Tyr Phe

100 105 110

Asp Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly Tyr Arg

115 120 125

Val Ser Pro Arg Cys Glu Tyr Gln Ala Gly His Asn Lys Val Gly Ser

130 135 140

Leu Gln Tyr Leu Ala Leu Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys

145 150 155 160

Pro Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys

165 170 175

Pro Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His

180 185 190

<210> 24

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 24

Ile Glu Trp Arg Lys Lys Arg Tyr

1

5

<210> 25

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 25

Asp Arg Trp Asn Lys Pro Gln

1

5

<210> 26

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 26

Ser Leu Gln Tyr Leu Ala

1

5

<210> 27

<211> 579

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 27

atggaaaaca gatggcaggt gattattgtg tggcaggtag acaggatgag gattagaaca 60
 tggacacgtt tagtaaaata ccatatgtat tgaatcaaga aagctaggga atggttttat 120
 tgacatcact atcaaaagtc tcatccaaaa gtaagttcag aagtacacat cccactagag 180
 gatgctagat tggaaataac atcatattgg ggtctgcata caggagaaaag agactggcat 240
 ttgggtcagg gagtctccat agaattggagg aaaaggagat atagcacaca cgtcgacct 300
 gatctagcag accaactaat tcatctgtat tattttgatt gttttcaga atctgctata 360
 agaaaagcca tattaggaca cagagttagt cctagggtgtg aatctgagc aggacatagc 420
 aaggttagat cactacagta ctggcaata gcagcattaa taacaccaa aaagataaag 480
 ccaccttgg cgagtgtcag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
 aagggccaca gagggagcca tacaatgaat ggacactag 579

<210> 28

<211> 579

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 28

atggaaaaca gatggcaggt gatgattgtg tggcaggtag acaggatgag gattagaaca 60
 tggacacgtt tagtaaaata ccatatgtat agatcaaga aagctaggga atggttttat 120
 agacatcact atcaaaagtc tcatccaaga gtaagttcag aagtacacat cccactagag 180
 gatgctagat tggaaataac aacatattgg ggtctgcata caggagaaaag agactggcat 240
 ttgggtcagg gagtctccat agaattggagg aaaaggagat atagcacaca agtagacct 300
 gatctagcag accaactaat tcatctgtat tattttgatt gttttcaga atctgctata 360
 agaaaagcca tattaggaca cagagttagt cctagggtgtg aatctgagc aggacatagc 420
 aaggttagat cactacagta ctggcaata gcagcattaa taacaccaa aaagataaag 480
 ccaccttgg cgagtgtcag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
 aagggccaca gagggagcca tacaatgaat ggacactag 579

<210> 29

<211> 579

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 29

atggaaaaca gatggcaggt gatgattgtg tggcaggtag acaggatgag gattagaaca 60
 tggacacgtt tagtaaaata ccatatgtat agatcaaga aagctaggga atggttttat 120
 agacatcact atcaaaagtc tcatccaaaa gtaagttcag aagtacacat cccactagag 180
 gatgctagat tggaaataac aacatattgg ggtctgcata caggagaaaag agactggcat 240
 ttgggtcagg gagtctccat agaattggagg aaaaggagat atagcacaca agtagacct 300

gatctagcag accaactaat tcactgtat tatittgatt gtitttcaga atctgctata 360
 agaaaagcca tattaggaca cagagttagt cctaggtgtg aatctgagc aggacatagc 420
 aaggtaggat cactacagta ctgggaata gcagcattaa taacacaaa aaagataaag 480
 ccactttgc cgagtgtcag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
 aagggccaca gaggagcca tacaatgaat ggacactag 579

<210> 30

<211> 579

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 30

atggaanaa gatggcaggt gatgattgtg tggcaggtag acaggatgag gattagaaca 60
 tggaaacagt tagtaacata ccatatgtat agatcacaga aagctaggga atgtttta 120
 agacatcact atcacagtcc tcactcaaaa gtaagttcag aagtcacat ccactagag 180
 gatgctagat tggcaatacc aacattttgg ggtctgcata caggagaaag agactggcat 240
 ttgggtcagg gagtctccat agaattggagg aaaaggagat atagcacaca agtagacct 300
 gatctagcag accaactaat tcactgtat tatittgatt gtitttcaga atctgctata 360
 agaaaagcca tattaggaca cagagttagt cctaggtgtg aatctgagc aggacatagc 420
 aaggtaggat cactacagta ctgggaata gcagcattaa taacacaaa aaagataaag 480
 ccactttgc cgagtgtcag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
 aagggccaca gaggagcca tacaatgaat ggacactag 579

<210> 31

<211> 579

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 31

atggaanaa gatggcaggt gatgattgtg tggcaggtag acaggatgag gattagaaca 60
 tggaaacagt tagtaaaata ccatatgtat agatcaaaga aagctaggga atgtttta 120
 agacatcact atcaaagtc tcactcaaaa gtaagttcag aagtcacat ccactagag 180
 gatgctagat tggaaataac aacatattgg ggtctgcata caggagaaag agactggcat 240
 ttgggtcagg gagtctccat agaattggagg aaaaggagat atagcacaca cgtgacct 300
 gatctgcag accaccta attcactgtat tatittgatt gtitttcaga atctgctata 360
 agaaaagcca tattaggaca cagagttagt cctaggtgtg aatctgagc aggacatagc 420
 aaggtaggat cactacagta ctgggaata gcagcattaa taacacaaa aaagataaag 480
 ccactttgc cgagtgtcag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
 aagggccaca gaggagcca tacaatgaat ggacactag 579

<210> 32
<211> 579
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Novel Sequence

<400> 32
atggaaaaca gatggcaggt gatgatttg tggcaggtag acaggatgag gattagaaca 60
tggaaacagt tagtaaaata ccatatgtat agatcaaaga aagctaggga atggttttat 120
agacatcact atcaaagtcc tcatccaaaa gtaagttcag aagtacacat cccactagag 180
gatgctagat tggtaataac aacatatggg ggctctgcata caggagaaag agactggcat 240
ttgggtcagg gagtctccat agaatggagg aaaaggagat atagcacaca cgtagacct 300
gatctagcag accaactaat tcatctgtat tattttgatt gttttcaga atctgctata 360
agaaaagcca tattaggaca cagagttagt ctaggtgtg aatatcgagc aggacatagc 420
aaggtaggat cactacagta cttggcaata gcagcattaa taacaccaa aaagataaag 480
ccacctttgg cgagtgtcag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
aagggccaca gaggagcca tacaatgaat ggacactag 579

<210> 33
<211> 579
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Novel Sequence

<400> 33
atggaaaaca gatggcaggt gatgatttg tggcaggtag acaggatgag gattagaaca 60
tggaaacagt tagtaaaata ccatatgtat agatcaaaga aagctaggga atggttttat 120
agacatcact atcaaagtcc tcatccaaaa gtaagttcag aagtacacat cccactagag 180
gatgctagat tggtaataac aacatatggg ggctctgcata caggagaaag agactggcat 240
ttgggtcagg gagtctccat agaatggagg aaaaggagat atagcacaca agtagacct 300
gatctagcag accacctaat tcatctgtat tattttgatt gttttcaga atctgctata 360
agaaaagcca tattaggaca cagagttagt ctaggtgtg aatatcgagc aggacatagc 420
aaggtaggat cactacagta cttggcaata gcagcattaa taacaccaa aaagataaag 480
ccacctttgg cgagtgtcag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
aagggccaca gaggagcca tacaatgaat ggacactag 579

<210> 34
<211> 579
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 34

atggaaaaca gatggcaggt gatgattgtg tggcaggtag acaggatgag gattagaaca 60
tggacacgtt tagtaaaata ccatatgtat agatcaaaaga aagctaggga atggtttat 120
agacatcact atcaaaagtc tcatccaaaa gtaagttcag aagtacacat cccactagag 180
gatgctagat tggtaataac aacattttgg ggctgcata caggagaaag agactggcat 240
ttggctcagg gagtctccat agaattggagg aaaaggagat atagcacaca cgtagacct 300
gatctagcag accaactaat tcatctgtat tattttgatt gttttcaga atctgctata 360
agaaaagcca tattaggaca cagagttagt cctaggtgtg aatatcgagc aggacatagc 420
aaggtaggat cactacagta ctggcaata gcagcattaa taacaccaa aaagataaag 480
ccacctttgc cgagtgtcag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
aagggtcaca gagggagcca tacaatgaat ggacactag 579

<210> 35

<211> 579

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 35

atggaaaaca gatggcaggt gatgattgtg tggcaggtag acaggatgag gattagaaca 60
tggacacgtt tagtaaaata ccatatgtat agatcaaaaga aagctaggga atggtttat 120
agacatcact atcacgtccc tcatccaaaa gtaagttcag aagtcacat cccactagag 180
gatgctagat tggaaataac aacattttgg ggctgcata caggagaaag agactggcat 240
ttggctcagg gagtctccat agaattggagg aaaaggagat atagcacaca agtagacct 300
gatctagcag accaactaat tcatctgtat tattttgatt gttttcaga atctgctata 360
agaaaagcca tattaggaca cagagttagt cctaggtgtg aatatcgagc aggacatagc 420
aaggtaggat cactacagta ctggcaata gcagcattaa taacaccaa aaagataaag 480
ccacctttgc cgagtgtcag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
aagggccaca gagggagcca tacaatgaat ggacactag 579

<210> 36

<211> 584

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 36

atggaaaaca gatggcaggt gatgattgtg tggcaggtag acaggatgag gattagaaca 60

tggaacagtt tagtaaaata ccatatgtat tgatcaaga aaagaagaa aggggaatggt 120
 ttatagaca tcactatcac agccctcacc cagaacaaag ttcaacagcc cacatccgc 180
 tagtggatgg tagatfgaa aaaatagcag ttggagctt ggatacagga gatggcgtct 240
 ggcacagggg gcacgagtc tccatagaat ggaggaaaag gagatagac acacaagtag 300
 accctgatct agtagacca ctaattcacc tgtattattt tgattgttt tcagaatcg 360
 ctataaaaa agccatatta ggacacagag ttatgctctg gtgtgaat cgagcaggag 420
 atagcaaggt aggcactact cagtactgg caatagcagc attaataaca ccaaaaaaga 480
 taagcccacc ttgccgagt gtcaggaaac tgacagagga tagatggaac aagcccaga 540
 agccaaggg ccacagaggg agccataca tgaatggaca ctac 584

<210> 37

<211> 579

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 37

atggaanaa gatggcaggt gatgattgt tggcaagtag acaggatgag gattagaaca 60
 tgaacagtt tagtaaaaca ccatatgtat gtttcaaga aagctaagaa atggtttat 120
 agacatcat atgaaagccc tcatcaaaa gtaagttcaa cagccacat cccgtaggg 180
 gatgctagat tggagaaaac agcagtttg agtctgcagg caggagatgg agcttgcac 240
 agggggcacc cagctccat agaattggagg aaaaggagat atagcacaca agtagacct 300
 gatgttgtag accaactaat tcatctgtat taatttgatt gttttcaga atctgctata 360
 agaaaagcca tattaggata tagagttagt cctaggtgtg aataccaagc aggcataat 420
 aaggtagat ctctacagta ctggcacta gcagcaltaa taacaccaaa gaagataaag 480
 ccactttgc ctagtgttag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
 aagggccaca gagggagcca tacaatgaat ggacactag 579

<210> 38

<211> 579

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 38

atggaanaa gatggcaggt gatgattgt tggcaagtag acaggatgag gattagagca 60
 tgaacagtt tagtaaaaca ccatatgtat gtttcaaga aagctaggac atggtttct 120
 agacatcat atggaagccc tcatcaaaa gtaagttcaa aagtaacat cccactaggg 180
 gatgctagat tggatgataa aacatattgg agtctgcatg caggagaaig agactggcat 240
 gtgggtcaga gactctccat agaattggagg aaaaggagat atagcacaca agtagacct 300
 gacttgcag accaactaat tcatctgtat taatttgatt gttttcaga atctgctata 360

agaaaagcca tattaggata tagagttagt cctaggtgtg aataccaagc aggacataat 420
aaggtaggat ctctacagta ctggcacta gcgacattaa taacaccaa gaagataaag 480
ccactttgc ctagtgtgag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
aagggccaca gagggagcca tacaatgaat ggacactag 579

<210> 39

<211> 579

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 39

atggaaaaca gatggcaggt gatgattgtg tggcaagtag acaggatgag gattagagca 60
tggacacgtt tagtaaaaca ccatatttt ttttcaaga aagctaagaa atggttttt 120
agacatcact atgaaagccc tcatccaaac gtaagttcag aagtacacat ccactaggg 180
gatgctagat tggtagaac accatattgg ggtctgcatg gaggagaaag agactggtat 240
ctggctcagg gagtctccat agaattggagg aaaaggagat atagcacaca agtagaccct 300
gacctggcag accaactaat tcatctgtat tattttgatt gttttcaga atctgctata 360
agaaaagcca tattaggata tagagttagt cctaggtgtg aataccaagc aggacataat 420
aaggtaggat ctctacagta ctggcacta gcgacattaa taacaccaa gaagataaag 480
ccactttgc ctagtgtgag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
aagggccaca gagggagcca tacaatgaat ggacactag 579

<210> 40

<211> 579

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 40

atggaaaaca gatgggaggt gatgattgtg tgggaagtag acaggatgag gattagagca 60
tggacacgtt tagtaaaaca ccatatgtat gtttcaaga aagctaagaa atggttttt 120
agacatcact atgaaagccc tcatccaaa gtaagttcag aagtacacat ccactaggg 180
gatgctagat tggtagaac aacatattgg ggtctgcatg caggagaaag agactggcat 240
ttgggtcagg gagtctccat agaattggagg aaaaggagat atagcacaca agtagaccct 300
gacctggcag accaactaat tcatctgtat tattttgatt gttttcaga atctgctata 360
agaaaagcca tattaggata tagagttagt cctaggtgtg aataccaagc aggacataat 420
aaggtaggat ctctacagta ctggcacta gcgacattaa taacaccaa gaagataaag 480
ccactttgc ctagtgtgag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
aagggccaca gagggagcca tacaatgaat ggacactag 579

<210> 41
<211> 579
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Novel Sequence

<400> 41
atggaaaaca gatggcaggt gatgattgtg tggcaagtag acaggatgag gattagagca 60
tggacacagt tagtaaaaca ccatatgtat gtttcaaaga acgctaagaa atggttttat 120
cgacatcact atgacagccc tcatccagtc caaagttcaa cagcccacat cccgctaggg 180
gatgtagat tgcagaaaa atgcatttgg agtctggatg caggagaaag agactggcat 240
ttgggtcagg gagtctccat agaattggagg aaaaggagat atagcacaca agtagaccct 300
gacctggcag accaactaat tcatctgtat tatittgatt gttttcaga atctgctata 360
agaaaagcca tattaggata tagagttagt ctaggtgtg aataccaagc aggacataat 420
aaggtaggat ctctacagta ctgggcacta gcagcattaa taacaccaa gaagataaag 480
ccacctttgc ctagtgtgag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
aaggggcaca gaggggagca tacaatgaat ggacactag 579

<210> 42
<211> 579
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Novel Sequence

<400> 42
atggaaaaca gatggcaggt gatgattgtg tggcaagtag acaggatgag gattagagca 60
tggacacagt tagtaaaaca ccatatgtat gtttcaaaga aagctaagaa atggttttat 120
agacatcact atgacagccc tcatccaaaa gtaagttcag aagtacacat cccactaggg 180
gatgctagat tggagataac aacatattgg ggtctgcatg caggagaaag agactggcat 240
ttgggtcagg gagtctccat agaattggagg aaaaggagat atagcacaca cgtagaccct 300
gacctggcag accaactaat tcatctgtat tatittgatt gttttcaga atctgctata 360
agaaaagcca tattaggata tagagttagt ctaggtgtg aataccaagc aggacataat 420
aaggtaggat ctctacagta ctgggcacta gcagcattaa taacaccaa gaagataaag 480
ccacctttgc ctagtgtgag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
aaggggcaca gaggggagca tacaatgaat ggacactag 579

<210> 43
<211> 579
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 43

atggaaaaca gatggcaggt gatgatttg tggcaagtag acaggatgac gattagagca 60
tggacacgtt tagtaaaaca ccatatgtat gtttcaaaga aagctaagaa atggtttat 120
agacatcaat atgaagccc tcatccaaaa gtaagttcag aagtaacat ccactaggg 180
gatgctagat tggtgataac aacattttgg ggtctgcatg caggagaaag agactggcat 240
ttgggtcagg gagtctccat agaattggagg aaaaggagat atagcacaca agtagacct 300
gacttggcag accaactaac tcatctgtat tattttgatt gttttcaga atctgctata 360
agaaaagcca tattaggata tagagttagt cctagggttg aataccaagc aggacataat 420
aaggtaggat ctctacagta ctggcacta gcgcatttaa taacacaaa gaagataaag 480
ccaccttgc ctagtgtgag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
aagggccaca gaggagacca tacaatgaat ggacactag 579

<210> 44

<211> 578

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 44

atggaaaaca gatggcaggt gatgatttg tggcaagtag acaggatgag gattagagca 60
tggacacgtt tagtaaaaca ccatatgtat gtttcaaaga aagctaagaa atggtttaa 120
agacatcaat atgaccgcc tcatccaaaa gtaagttcag aagtcacat ccactaggg 180
gatgctagat tggagataac aacattttgg ggtctgcatg caggagaaag agactggcat 240
ttgggtcagg gagtctccat agaattggagg aaaaggagat atagcacaca agtagacct 300
gacttggcag accaactaac tcatctgtat tattttgatt gttttcaga atctgctata 360
agaaaagcca tattaggata tagagttagt cctagggttg aataccaagc aggacataat 420
aaggtaggat ctctacagta ctggcacta gcgcatttaa taacacaaa gaagataaag 480
ccaccttgc ctagtgtgag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
aagggccagc agggagccat acaatgaatg gacactag 578

<210> 45

<211> 579

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 45

atggaaaaca gatggcaggt gatgatttg tggcaagtag acaggatgag gattagagca 60

tggacacagt tagtaaaaca ccatatgttt gtttcaaaga aagctaagaa atggttttat 120
 agacatcact atgaaagccc tcatccaaaa gtaagttcag aagtaacat cccactaggg 180
 gatgctagat tggagataac aacattttgg ggtctgcatg caggagaaag agactggcat 240
 ttgggtcagg gagtctccat agaattggagg aaaaggagat atagcacaca agtagacct 300
 gacctggcag accaactaat tcatctgtat tattttggtt gttttcaga atctgctata 360
 agaaaagcca tattaggata tagagttagt cctaggtgtg aataccaagc aggacataat 420
 aagftaggat ctctacagta ctgggacta gcagcattaa taacaccaa gaagataaag 480
 ccactttgc ctagtgtgag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
 aagggccaca gagggagcca tacaatgaat ggacactag 579

<210> 46

<211> 579

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 46

atggaaaca gatggcaggt gatgattgtg tggcaagtag acaggatgag gattagagca 60
 tggacacagt tagtaaaaca ccatatgtat gtttcaaaga aagctaagaa atggttttat 120
 agacatcact atgaaagccc tcatccaaa gtaagttcag aagtaacat cccactaggg 180
 gatgctagat tggagataac aacatattgg ggtctgcatg caggagaaag agactggcat 240
 ttgggtcagg gagtctccat agaattggagg aaaaggagat atagcacaca agtagacct 300
 gacctggcag accaactaat tcatctgtat tattttgatt gttttcaga atctgctata 360
 agaaaagcca tattaggata tagagttagt cctaggtgtg aataccaagc aggacataat 420
 aagftaggat ctctacagta ctgggacta gcagcattaa taacaccaa gaagataaag 480
 ccactttgc ctagtgtgag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
 aagggccaca gagggagcca tacaatgaat ggacactag 579

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ATTENUATED VIF DNA IMMUNIZATION CASSETTES
FOR GENETIC VACCINES

ACKNOWLEDGMENT OF GOVERNMENT RIGHTS

This invention was made with Government support from the National
5 Institutes of Health. The Government has certain rights in this invention.

FIELD OF THE INVENTION

The invention relates to the preparation and use of attenuated, nonfunctional
HIV *vif* immunization cassettes as genetic vaccines for pathogenic genes.

BACKGROUND OF THE INVENTION

10 Vaccination and immunization generally refer to the introduction of a non-
virulent agent against which an individual's immune system can initiate an immune response
which will then be available to defend against challenge by a pathogen. The immune system
identifies invading "foreign" compositions and agents primarily by identifying proteins and
other large molecules which are not normally present in the individual. The foreign protein
15 represents a target against which the immune response is made.

The immune system can provide multiple means for eliminating targets that
are identified as foreign. These means include humoral and cellular responses which
participate in antigen recognition and elimination. Briefly, the humoral response involves B
cells which produce antibodies that specifically bind to antigens. There are two arms of the
20 cellular immune response. The first involves helper T cells which produce cytokines and

elicit participation of additional immune cells in the immune response. The second involves killer T cells, also known as cytotoxic T lymphocytes (CTLs), which are cells capable of recognizing antigens and attacking the antigen including the cell or particle it is attached to.

Vaccination has been singularly responsible for conferring immune protection
5 against several human pathogens. In the search for safe and effective vaccines for immunizing individuals against infective pathogenic agents such as viruses, bacteria, and infective eukaryotic organisms, several strategies have been employed thus far. Each strategy aims to achieve the goal of protecting the individual against pathogen infection by administering to the individual, a target protein associated with the pathogen which can elicit
10 an immune response. Thus, when the individual is challenged by an infective pathogen, the individual's immune system can recognize the protein and mount an effective defense against infection. There are several vaccine strategies for presenting pathogen proteins which include presenting the protein as part of a non-infective or less infective agent or as a discreet protein composition.

15 One strategy for immunizing against infection uses killed or inactivated vaccines to present pathogen proteins to an individual's immune system. In such vaccines, the pathogen is either killed or otherwise inactivated using means such as, for example, heat or chemicals. The administration of killed or inactivated pathogen into an individual presents the pathogen to the individual's immune system in a noninfective form and the individual can
20 thereby mount an immune response against it. Killed or inactivated pathogen vaccines provide protection by directly generating T-helper and humoral immune responses against the pathogenic immunogens. Because the pathogen is killed or otherwise inactivated, there is little threat of infection.

Another method of vaccinating against pathogens is to provide an attenuated
25 vaccine. Attenuated vaccines are essentially live vaccines which exhibit a reduced infectivity. Attenuated vaccines are often produced by passaging several generations of the pathogen through a permissive host until the progeny agents are no longer virulent. By using an attenuated vaccine, an agent that displays limited infectivity may be employed to elicit an immune response against the pathogen. By maintaining a certain level of infectivity, the
30 attenuated vaccine produces a low level infection and elicits a stronger immune response than killed or inactivated vaccines. For example, live attenuated vaccines, such as the poliovirus

and smallpox vaccines, stimulate protective T-helper, T-cytotoxic, and humoral immunities during their nonpathogenic infection of the host.

Another means of immunizing against pathogens is provided by recombinant vaccines. There are two types of recombinant vaccines: one is a pathogen in which specific genes are deleted in order to render the resulting agent non-virulent. Essentially, this type of recombinant vaccine is attenuated by design and requires the administration of an active, non-virulent infective agent which, upon establishing itself in a host, produces or causes to be produced antigens used to elicit the immune response. The second type of recombinant vaccine employs infective non-virulent vectors into which genetic material that encode target antigens is inserted. This type of recombinant vaccine similarly requires the administration of an active infective non-virulent agent which, upon establishing itself in a host, produces or causes to be produced, the antigen used to elicit the immune response. Such vaccines essentially employ infective non-virulent agents to present pathogen antigens that can then serve as targets for an anti-pathogen immune response. For example, the development of vaccinia as an expression system for vaccination has theoretically simplified the safety and development of infectious vaccination strategies with broader T-cell immune responses.

Another method of immunizing against infection uses subunit vaccines. Subunit vaccines generally consist of one or more isolated proteins derived from the pathogen. These proteins act as target antigens against which an immune response may be mounted by an individual. The proteins selected for subunit vaccine are displayed by the pathogen so that upon infection of an individual by the pathogen, the individuals immune system recognizes the pathogen and mounts a defense against it. Because subunit vaccines are not whole infective agents, they are incapable of becoming infective. Thus, they present no risk of undesirable virulent infectivity that is associated with other types of vaccines. It has been reported that recombinant subunit vaccines such as the hepatitis B surface antigen vaccine (HBsAg) stimulate a more specific protective T-helper and humoral immune response against a single antigen. However, the use of this technology to stimulate broad protection against diverse pathogens remains to be confirmed.

The construction of effective vaccines is complicated by several factors which include the pathobiology of the pathogen and the specificities of the of the host immune response. Recently a novel tool for understanding the immune component in these

interactions has become available in the form of genetic immunization or DNA vaccination. Tang, *et al.*, *Nature*, **1992**, 356, 152; Fynan, *et al.*, *Proc. Natl. Acad. Sci. USA*, **1993**, 90, 11478; Ulmer, *et al.*, *Science*, **1993**, 259, 1745; and Wang, *et al.*, *Proc. Natl. Acad. Sci. USA*, **1993**, 90, 4156. The ability of this approach was demonstrated to produce broad immune responses against structural and enzymatic gene products of HIV-1 and outlined a strategy for development of a possible prophylactic vaccine for HIV-1. This strategy utilized multiple gene expression cassettes encoding *gag/pol/rev* as well as *env/rev* and accessory gene immunogens. Studies clearly demonstrated that rodents and primates can be successfully immunized with HIV-1 structural and envelope genes. Wang, *et al.*, *Proc. Natl. Acad. Sci. USA*, **1993**, 90, 4156 and Wang, *et al.*, *DNA Cell Biol.*, **1993**, 12, 799. A genetic strategy for construction of immunogen expression cassettes from a pathogenic gene which can be broadly applied in order to use DNA immunogens against a variety of pathogens is needed.

Primate lentiviral genomes contain genes encoding novel regulatory and accessory proteins as well as proteins with structural and enzymatic functions. The regulatory genes, *tat* and *rev*, and the accessory genes, *nef*, *vif*, *vpr*, *vpu*, and *vpx*, are well conserved in many lentiviruses, including HIV and SIV. The well conserved nature of these genes implies that their protein products play a critical role in viral pathogenesis *in vivo*. Initial *in vitro* experiments seemed to demonstrate that *tat* and *rev* were essential for viral replication, while the accessory genes were considered nonessential. Cullen, *et al.*, *Cell*, **1989**, 58, 423 and Desrosiers, *AIDS Res. Human Retroviruses*, **1992**, 8, 411. Further analyses, however, has revealed that defects within the accessory gene result in severe impairment or delay in viral replication *in vitro* (Gabudza, *et al.*, *J. Virol.*, **1992**, 66, 6489 and Gibbs, *et al.*, *AIDS Res. Human Retroviruses*, **1994**, 10, 343) and *in vivo* (Aldrovandi, *et al.*, *J. Virol.*, **1996**, 70, 1505). Native defective accessory genes have been reported *in vivo* and may be an end product of an effective host immune response. The accessory genes are, therefore, presently considered to be determinants of virus virulence. Trono, *Cell*, **1995**, 82, 189. They contain few "hot spots" and may be less susceptible to mutations leading to the production of "escape" virus variants, emphasizing their importance in the viral life cycle. In addition, the protein products of these genes are immunogenic *in vivo*. As a group, they represent twenty percent of the possible anti-viral immune targets. Ameisen, *et al.*, *Int. Conf. AIDS*, **1989**, 5, 533 and Lamhamedi-Cherradi, *et al.*, *AIDS*, **1992**, 6, 1249. Their immunogenicity and low functional

mutagenicity combine to make the accessory genes attractive elements in the design of future anti-viral immune therapeutics. The production of accessory gene immunogens poses specific immunologic and pathogenic complications for a viral vaccine design, however, due to the role of the accessory gene protein products as determinants of viral virulence. A potential accessory gene-based genetic vaccine would need to be accessible to the host's immune response against native viral accessory gene products without enhancing viral replication. Accordingly, a major goal is to design a safe and effective genetic anti-HIV vaccine, which includes the *vif* (virion infectivity factor) accessory gene as part of a multi-component genetic immunogen.

The *vif* gene encodes a 23 kDa late viral protein (*vif*) from a singly spliced, rev-dependent 5 kb transcript. Arya, *et al.*, *Proc. Natl. Acad. Sci. USA*, **1986**, 83, 2209; Garrett, *et al.*, *J. Virol.*, **1991**, 65, 1653; Schwartz, *et al.*, *Virol.*, **1991**, 183, 677; and Sodroski, *et al.*, *Science*, **1986**, 231, 1549. *Vif* is highly conserved among HIV-1 isolates and is present in other lentiviruses, such as Feline Immunodeficiency Virus (FIV), Bovine Immunodeficiency Virus (BIV), Visna virus, HIV-2, and SIV. Myers, *et al.*, *Human Retrovir. AIDS*, **1991** and Shackett, *et al.*, *Virol.*, **1994**, 204, 860. Earlier analyses of *in vivo vif* genetic variation have shown that most *vif* sequences are intact reading frames and the presence of intact *vif* does not have a correlation with disease status. Sova, *et al.*, *J. Virol.*, **1995**, 69, 2557 and Wieland, *et al.*, *Virol.*, **1994**, 203, 43. However, sequential analyses of a region containing *vif*, *vpr*, *vpu*, *tat*, and *rev* genes from a HIV-1 infected long-term progressor revealed the presence of inactivating mutations in 64% of the clones. Michael, *et al.*, *J. Virol.*, **1995**, 69, 4228. HIV-1 infected subjects have been shown to carry antibodies which recognize recombinant *vif* protein (Kan, *et al.*, *Science*, **1986**, 231, 1553; Schwander, *et al.*, *J. Med. Virol.*, **1992**, 36, 142; and Wieland, *et al.*, *AIDS Res. Human Retrovir.*, **1991**, 7, 861) suggesting that the protein is expressed and is immunogenic during natural infection (Volsky, *et al.*, *Curr. Topics Micro. Immunol.*, **1995**, 193, 157.

Due to *vif*'s ability to activate viral replication in *trans*, an attenuated genetic vaccine design, similar to those utilized in the production of vaccines derived from toxic viral, bacterial, or parasitic components was employed in the present invention. The sequence variation and immunogenic potential present in *vif* genes derived from HIV-1 infected subjects was analyzed. Prototypic genetic variants were selected and the ability of those

clones to induce humoral and cellular immune responses was studied in animals. The selected *vif* genetic variants were also functionally characterized through transcomplementation assays utilizing cells infected with a *vif*-defective HIV-1 clone. Attenuated, nonfunctional *vif* clones are demonstrated to induce immune responses capable of destroying native pathogen.

5 SUMMARY OF THE INVENTION

The present invention relates to a purified attenuated, non-functional *vif* protein.

The present invention relates to a *vif* protein comprising an amino acid sequence selected from the group consisting of SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, and SEQ ID NO:23.

The present invention relates to an isolated nucleic acid molecule comprising a nucleotide sequence encoding an attenuated, non-functional *vif* protein.

The present invention relates to a nucleic acid molecule encoding a *vif* protein which comprises an amino acid sequence selected from the group consisting of SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22 and SEQ ID NO:23.

The present invention relates to a nucleic acid molecule encoding a *vif* protein which comprises a nucleotide sequence selected from the group consisting of SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45 and SEQ ID NO:46.

The present invention relates to a pharmaceutical composition comprising the nucleic acid molecule encoding an attenuated, non-functional *vif* protein in a pharmaceutically acceptable carrier or diluent.

The present invention relates to a recombinant expression vector comprising a nucleic acid molecule comprising a nucleotide sequence encoding an attenuated, non-functional *vif* protein.

The present invention relates to a host cell comprising a recombinant
5 expression vector comprising a nucleic acid molecule encoding an attenuated, non-functional *vif* protein

The present invention relates to a purified antibody directed against an attenuated, non-functional *vif* protein.

The present invention relates to a method of immunizing a mammal against
10 a virus comprising administering to cells of said mammal, a nucleic acid molecule that comprises a nucleotide sequence that encodes an attenuated, non-functional *vif* protein, wherein said nucleic acid molecule is expressed in said cells.

BRIEF DESCRIPTION OF THE FIGURES

Figure 1 shows a comparison of the deduced amino acid sequences of *vif*
15 derived from transmitter and non-transmitter mothers with well characterized HIV-1 molecular clones PNL43, SF-2, and Zr6. T-#, clones from transmitter subject; N-#, clones from non-transmitter subject; --, identity with the consensus sequence (Con; SEQ ID NO:1), ..., represents gap; *, a stop codon.

Figure 2 shows a 10% SDS-PAGE of immunoprecipitates. Expression of
20 HIV-1 *vif* clones derived from transmitter and non-transmitter mothers. *Vif* expression plasmids were used for coupled *in vitro* transcription/translation according to the manufacturer's instructions (Promega). Immunoprecipitation of the *in vitro* translated proteins was performed with *vif* antiserum as described herein. The designation of the *vif* clones is indicated on the top. The clone numbers designated with T-** and N-** are derived
25 from the transmitter and non-transmitter mothers respectively. pCVif is the *vif* expression plasmid of HIV-1_{SF2}.

Figures 3A and 3B show the results of an enzyme linked immunoabsorbent assay (ELISA) of anti-*vif* antibody responses in mice after immunization with a DNA construct expressing *vif*. Mouse sera was diluted in blocking buffer at a dilution of 1:500 and

assayed as described herein. In Figure 3A, mice were immunized with 50 µg of DNA. In Figure 3B, mice were immunized with 100 µg of DNA per injection.

Figure 4 shows the results of a chromium release assay whereby lysis of murine targets (p815) expressing *vif* protein by splenocytes from mice immunized with *vif* expression constructs. p815 cells (1×10^5 /ml) were infected with vaccinia expressing *vif* (VV:gag) and incubated for 16 hours to express the Vif protein. The target cells were labeled with ^{51}Cr for 1-2 hours and used to incubate the stimulated splenocytes for 6 hours. Specific lysis (%) was calculated according to the formula described herein.

Figures 5A, 5B, 5C and 5D show the results of a chromium release assay whereby lysis of HeLa CD4+/D^d cells infected with clinical HIV-1 isolate by splenocytes from mice immunized with *vif* expression cassette. HeLa CD4+/D^d cells (10^6) were infected with cell-free HIV-1 clinical isolate followed by a week incubation to allow the cells to infect and express viral proteins. One week postinfection, the target cells were labeled with ^{51}Cr for 1-2 hours and used to incubate the stimulated splenocytes for 6 hours. Specific lysis (%) was calculated according to the formula described herein.

Figure 6 shows the results of a proliferation assay showing activation and T cell proliferative response to recombinant Vif. Recombinant Vif (10 µg/ml) was plated in each well to stimulate proliferation of T cells. Lectin PHA (10 µg/ml) was used as a polyclonal stimulator positive control. Stimulation index was calculated as the level of radioactivity detected from the cells stimulated with specific protein divided by the level detected from the cells in media. Lanes 1a and 1b are from mice immunized with 50 and 100 µg of pCVif; Lanes 2a and 2b are from mice immunized with 50 and 100 µg of clone T-35; Lanes 2a and 2b are from mice immunized with 50 and 100 µg of clone N-15.

Figures 7A-7F show the amino acid sequences of preferred attenuated, non-functional *vif* proteins of the present invention.

Figures 8A-8E show the nucleotide sequences of preferred attenuated, non-functional *vif* proteins of the present invention.

DETAILED DESCRIPTION OF THE INVENTION

One of the major goals of AIDS research is the development of a vaccine against the HIV-1 virus. An effective vaccine should elicit strong humoral response along

with an efficient and broad CTL response. This task is complicated because of the genetic heterogeneity of the HIV-1 virus. HIV-1 reverse transcriptase (RT) is prone to error and lacks the ability to proof-read, resulting in a mutation rate of 10^{-4} per cycle per genome.

Dougherty, *et al.*, *J. Virol.*, **62**, 2817. HIV-1 genome sequence variation has been observed

- 5 in viruses isolated from different individuals as well as in virus isolated from a single person at different time points. Fisher, *et al.*, *Nature*, **1988**, 334, 444 and Meyerhans, *et al.*, *Cell*, **1989**, 58, 901. Based upon a large number of sequence analysis data, it is apparent that the structural genes *env*, *gag* and *pol* are the major target for mutations which lead to escape-variant viruses in patients by changing the neutralizing antibody and/or CTL epitopes.
- 10 Pircher, *et al.*, *Nature*, **1990**, 346, 629; Reitz, *et al.*, *Cell*, **1988**, 54, 57; and Wolfs, *et al.*, *Virol.*, **1991**, 185, 195. Despite this, earlier experiments have indicated that structural and enzymatic genes of HIV-1 can be used successfully as nucleic acid-based vaccines in different animal models (Wang, *et al.*, *Proc. Natl. Acad. Sci. USA*, **1993**, 90, 4156; and Wang, *et al.*, *AIDS*, **1995**, 9 (Suppl A), S159) and prophylactic as well as therapeutic studies for DNA
- 15 vaccines have commenced. The present invention is directed to development of *vif*, a HIV-1 accessory gene, as an immunogen cassette. When used in concert with other HIV-1 genes a broad immune response against all viral components may be induced, thus mimicking many aspects of the immune responses induced by a live attenuated vaccine.

- In the present invention, induction of *vif*-specific humoral and cellular immune
- 20 responses in mice have been observed to directly correlate with the concentration of DNA injected and number of boosts. Similar results were observed in T-cell proliferation and CTL assays, demonstrating that *vif* genes are immunogenic *in vivo*. *Vif* is known to present in both soluble and membrane associated form. Goncalves, *et al.*, *J. Virol.*, **1994**, 68, 704. Although anti-*vif* antibodies and *vif*-specific CTL responses have been shown in HIV-1 positive
- 25 patients, epitopes involved in the presentation of *vif* to the immune system have not yet been defined. Lamhamedi-Cherradi, *et al.*, *AIDS*, **1992**, 6, 1249. How *vif* becomes exposed to the humoral immune system is unclear in these studies. The observed different immune response in the clones of the present invention suggest that the mutations in T-35, N-15 and pCVif may be associated with changes in antibody/CTL responses.

- 30 It is significant to note that some the point mutations present in all the T or N derived clones indicate that these mutations may be responsible for the difference in

complementation and/or immune responses observed. Further mutational analysis of *vif* help resolve answer the regions involved in complementation. Proposed sites of *vif* activity include viral DNA synthesis, *gpl20* synthesis and transport, and gag processing. Borman, *et al.*, *J. Virol.*, **1995**, 69, 2058; Sakai, *et al.*, *J. Virol.*, **1993**, 67, 1663; and Von Schwedler, *et al.*, *J. Virol.*, **1993**, 67, 4945. Transcomplementation experiments with *vif*-defective HIV-1 provirus and wild-type HIV-1 *vif*-expressing cell lines indicate that *vif* acts at a late stage in virus replication/maturation and that *vif* transcomplementation occurs across HIV-1 strains. Blanc, *et al.*, *Virol.*, **1993**, 193, 186 and Hevey, *et al.*, *Virus Res.*, **1994**, 33, 269. Earlier experiments have shown that sera from the nontransmitter subject (N1) contains a high antibody titer against envelope protein and nonreplicating virus; whereas sera from the transmitter patient (T1) contains very low antibody titers against envelop proteins and highly replicating virus. Velpandi, *et al.*, *DNA Cell Biol.*, **1996**, 15, 571. These results correlate with the trans-complementation results observed in the present invention.

The present invention relates to isolated nucleic acid molecules comprising a nucleotide sequence encoding an attenuated, non-functional *vif* protein. As used herein, the term "attenuated, non-functional *vif* protein" is meant to refer to *vif* proteins that have no or reduced virion infectivity function compared to wild-type *vif*. In some embodiments of the invention, the nucleic acid molecules encode an attenuated, non-functional *vif* protein wherein the nucleotide sequence comprises deletions, additions, a point mutation(s), multiple substitutions, or introduction of a stop codon to render a shortened protein. In preferred embodiments of the invention, the isolated nucleic acid molecules of the invention encode a *vif* protein comprising the amino acid sequence selected from the group consisting of SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22 and SEQ ID NO:23. In other preferred embodiments of the invention, the isolated nucleic acid molecules encode a *vif* protein and comprise a nucleotide sequence selected from the group consisting of SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID

NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45 and SEQ ID NO:46.

The nucleic acid molecules of the invention may be obtained from patients infected with the human immunodeficiency virus as described below in the Examples.

- 5 Alternatively, the nucleic acid molecules of the invention may be prepared using the wild-type *vif* nucleotide sequence. The *vif* expression plasmid, pCVif, contains the *vif* gene from the well-characterized HIV-1 molecular clone, pHXB2, under the control of the cytomegalovirus (CMV) immediate early promoter, within the backbone plasmid, pRc/CMV (Invitrogen, San Diego, CA) as described in Nagashunmugam, *et al.*, *DNA Cell Biol.*, **1996**,
10 15, 353, incorporated herein by reference. This nucleic acid molecule may be used to prepare additional nucleic acid molecules encoding attenuated, non-functional *vif* proteins.

- A number of methods can be used to design specific mutations in wild-type nucleic acid molecules to produce nucleic acid molecules encoding attenuated, non-functional *vif* proteins. For example, oligonucleotide-mediated mutagenesis is commonly used to add,
15 delete, or substitute nucleotides in a segment of DNA whose sequence is known. Such methods are taught in, for example, Sambrook et al., *Molecular Cloning a Laboratory Manual*, Second Ed. Cold Spring Harbor Press (1989), pages 15.51 to 15.73, which is incorporated herein by reference. Briefly, the protocol for oligonucleotide-mediated mutagenesis involves the following steps: 1) cloning of an appropriate fragment of DNA,
20 such as the *vif* nucleotide sequence from the pCVif expression plasmid, into a bacteriophage M13 vector; 2) preparation of single-stranded DNA from the recombinant bacteriophage M13; 3) design and synthesis of mutagenic oligonucleotides; 4) hybridization of the mutagenic oligonucleotides to the target DNA; 5) extension of the hybridized oligonucleotide by DNA polymerase; 6) transfection of susceptible bacteria; 7) screening of bacteriophage
25 plaques for those carrying the desired mutation; 8) preparation of single-stranded DNA from the mutagenized recombinant bacteriophage; 9) confirmation by sequencing that the mutagenized bacteriophage M13 DNA carries the desired mutation and no other mutation; 10) recovery of the mutated fragment of DNA from the double-stranded replicative form of the recombinant bacteriophage M13; and 11) substitution of the mutagenized fragment for
30 the corresponding segment of wild-type DNA in the desired expression vector.

Design and synthesis of the mutagenic oligonucleotides, which are tailored to the desired mutation in the nucleic acid molecule encoding *vif*, is described in detail in, for example, Sambrook et al., *Molecular Cloning a Laboratory Manual*, Second Ed. Cold Spring Harbor Press (1989), pages 15.54 to 15.56, which is incorporated herein by reference. For example, to substitute, add, or delete a single nucleotide into the wild-type *vif* nucleotide sequence, oligonucleotides of about 17-19 nucleotides in length which carry the mismatched nucleotide at the center or at one of the two nucleotide positions immediately 3' of the center are prepared. To substitute, add, or delete two or more contiguous nucleotides into the wild-type *vif* nucleotide sequence, oligonucleotides of about 25 or more nucleotides in length are prepared. These oligonucleotides comprise about 12 to 15 perfectly matched nucleotides on either side of the central looped-out region which contains the added or substituted nucleotides, or represents the portion of the wild-type DNA that is looped out. Using the strategy described above, one skilled in the art can prepare nucleic acid molecules having deletions, additions, substitutions, or premature stop codons, which encode attenuated, non-functional *vif* proteins. Oligonucleotide-mediated mutagenesis procedures are widely known to those skilled in the art.

Alternately, the nucleic acid molecules of the invention can be prepared using DNA synthesizers by standard DNA methodology. One skilled in the art readily understands that the genetic code is degenerate and, therefore, could prepare numerous DNA sequences encoding the same protein. In addition, one skilled in the art readily understands that amino acids can be substituted by other amino acids such that conservative substitutions are made. Accordingly, one skilled in the art can prepare nucleic acid molecules of the invention encoding attenuated, non-functional *vif* proteins.

Preferred nucleic acid molecules of the invention encode attenuated, non-functional *vif* proteins having the amino acid (a.a.) and nucleotide sequences (nt.) (represented by particular SEQ ID Numbers) in Table 1. The specific amino acid sequences are shown in Figure 1 and Figures 7A-7F. The specific nucleotide sequences are shown in Figures 8A-8E.

Table 1

	Vif Protein	SEQ ID	NO:	Vif Protein	SEQ ID	NO:
		a.a.	nt.		a.a.	nt.
	N13	4	27	T3	14	37
	N15	5	28	T4	15	38
5	N17	6	29	T35	16	39
	N22	7	30	T37	17	40
	N23	8	31	T38	18	41
	N24	9	32	T39	19	42
	N26	10	33	T40	20	43
10	N27	11	34	T42	21	44
	N29	12	35	T43	22	45
	N30	13	36	T44	23	46

The present invention also relates to vectors or recombinant expression vectors that comprise a nucleotide sequence that encodes an attenuated, non-functional *vif* protein.

- 15 As used herein, the term "recombinant expression vector" is meant to refer to a plasmid, phage, viral particle or other vector which, when introduced into an appropriate host, contains the necessary genetic elements to direct expression of the coding sequence that encodes an attenuated, non-functional *vif* protein. In some embodiments of the invention, the vector or recombinant expression vector encodes an attenuated, non-functional *vif* protein wherein the
- 20 nucleotide sequence comprises deletions, additions, point mutation(s), multiple substitutions, or introduction of a stop codon to render a shortened protein. In preferred embodiments of the invention, the vectors or recombinant expression vectors of the invention encode a *vif* protein comprising the amino acid sequence selected from the group consisting of SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID
- 25 NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22 and SEQ ID NO:23. In other preferred embodiments of the invention, the vectors or recombinant expression vectors of the invention comprise a nucleic

acid molecule encoding a *vif* protein which comprises a nucleotide sequence selected from the group consisting of SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45 and SEQ ID NO:46.

One having ordinary skill in the art can isolate the nucleic acid molecule that encodes an attenuated, non-functional *vif* protein and insert it into an expression vector using standard techniques and readily available starting materials. The coding sequence is operably linked to the necessary regulatory sequences. Expression vectors are well known and readily available. Examples of expression vectors include plasmids, phages, viral vectors and other nucleic acid molecules or nucleic acid molecule containing vehicles useful to transform host cells and facilitate expression of coding sequences. The recombinant expression vectors of the invention are useful for transforming hosts which express an attenuated, non-functional *vif* protein.

The present invention also relates to a host cell that comprises the recombinant expression vector that includes a nucleotide sequence that encodes an attenuated, non-functional *vif* protein. In some embodiments of the invention, the host cell comprises the vector or recombinant expression vector that encodes an attenuated, non-functional *vif* protein wherein the nucleotide sequence comprises deletions, additions, point mutation(s), multiple substitutions, or introduction of a stop codon to render a shortened protein. In preferred embodiments of the invention, the host cells comprises vectors or recombinant expression vectors that encode a *vif* protein comprising the amino acid sequence selected from the group consisting of SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22 and SEQ ID NO:23. In other preferred embodiments of the invention, the host cell comprises vectors that comprise a nucleotide sequence selected from the group consisting of SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45

and SEQ ID NO:46. Host cells for use in well known recombinant expression systems for production of proteins are well known and readily available.

The most commonly used prokaryotic system remains *E. coli*, although other systems such as *B. subtilis* and *Pseudomonas* are also useful. Suitable control sequences for prokaryotic systems include both constitutive and inducible promoters including the *lac* promoter, the *trp* promoter, hybrid promoters such as *tac* promoter, the *lambda* phage P1 promoter. In general, foreign proteins may be produced in these hosts either as fusion or mature proteins. When the desired sequences are produced as mature proteins, the sequence produced may be preceded by a methionine which is not necessarily efficiently removed.

10 Accordingly, the peptides and proteins claimed herein may be preceded by an N-terminal Met when produced in bacteria. Moreover, constructs may be made wherein the coding sequence for the peptide is preceded by an operable signal peptide which results in the secretion of the protein. When produced in prokaryotic hosts in this matter, the signal sequence is removed upon secretion. Examples of prokaryotic host cells include bacteria cells such as *E. coli*, and

15 yeast cells such as *S. cerevisiae*.

A wide variety of eukaryotic hosts are also now available for production of recombinant foreign proteins. As in bacteria, eukaryotic hosts may be transformed with expression systems which produce the desired protein directly, but more commonly signal sequences are provided to effect the secretion of the protein. Eukaryotic systems have the additional advantage that they are able to process introns which may occur in the genomic sequences encoding proteins of higher organisms. Eukaryotic systems also provide a variety of processing mechanisms which result in, for example, glycosylation, carboxy-terminal amidation, oxidation or derivatization of certain amino acid residues, conformational control, and so forth. Commonly used eukaryotic systems include, but are not limited to, yeast, fungal

20 cells, insect cells, mammalian cells, avian cells, and cells of higher plants. In preferred embodiments of the invention insect cells such as *S. frugiperda*, non-human mammalian tissue culture cells chinese hamster ovary (CHO) cells and human tissue culture cells such as HeLa cells are used as host cells. Suitable promoters are available which are compatible and operable for use in each of these host types as well as are termination sequences and

25 enhancers, as e.g. the baculovirus polyhedron promoter. As above, promoters can be either

30

constitutive or inducible. For example, in mammalian systems, the mouse metallothioneine promoter can be induced by the addition of heavy metal ions.

In some embodiments, for example, one having ordinary skill in the art can, using well known techniques, insert DNA molecules into a commercially available expression vector for use in well known expression systems. For example, the commercially available plasmid pSE420 (Invitrogen, San Diego, CA) may be used for production of an attenuated, non-functional *vif* protein in *E. coli*. The commercially available plasmid pYES2 (Invitrogen, San Diego, CA) may, for example, be used for production in *S. cerevisiae* strains of yeast. The commercially available MAXBAC™ complete baculovirus expression system (Invitrogen, San Diego, CA) may, for example, be used for production in insect cells. The commercially available plasmid pcDNA1 or pcDNA3 (Invitrogen, San Diego, CA) may, for example, be used for production in mammalian cells such as Chinese Hamster Ovary cells. One having ordinary skill in the art can use these commercial expression vectors and systems or others to produce an attenuated, non-functional *vif* protein by routine techniques and readily available starting materials. See e.g., Sambrook et al., *Molecular Cloning a Laboratory Manual*, Second Ed. Cold Spring Harbor Press (1989), which is incorporated herein by reference.

One having ordinary skill in the art may use other commercially available expression vectors and systems or produce vectors using well known methods and readily available starting materials. Expression systems containing the requisite control sequences, such as promoters and polyadenylation signals, and preferably enhancers, are readily available and known in the art for a variety of hosts. See e.g., Sambrook et al., *Molecular Cloning a Laboratory Manual*, Second Ed. Cold Spring Harbor Press (1989).

Examples of genetic constructs include the attenuated, non-functional *vif* protein coding sequence operably linked to a promoter that is functional in the cell line into which the constructs are transfected. Examples of constitutive promoters include promoters from cytomegalovirus or SV40. Examples of inducible promoters include mouse mammary leukemia virus or metallothionein promoters. Those having ordinary skill in the art can readily produce genetic constructs useful for transfecting with cells with DNA that encodes an attenuated, non-functional *vif* protein from readily available starting materials. Such gene constructs are useful for the production of an attenuated, non-functional *vif* protein.

Nucleic acid molecules that encode an attenuated, non-functional *vif* protein may be delivered to cells using any one of a variety of delivery components, such as recombinant viral expression vectors or other suitable delivery means, so as to affect their introduction and expression in compatible host cells. In general, viral vectors may be DNA
5 viruses such as recombinant adenoviruses and recombinant vaccinia viruses or RNA viruses such as recombinant retroviruses. Other recombinant vectors include recombinant prokaryotes which can infect cells and express recombinant genes. In addition to recombinant vectors, other delivery components are also contemplated such as encapsulation in liposomes, transferrin-mediated transfection and other receptor-mediated means. The invention is
10 intended to include such other forms of expression vectors and other suitable delivery means which serve equivalent functions and which become known in the art subsequently hereto.

In a preferred embodiment of the present invention, DNA is delivered to competent host cells by means of an adenovirus. One skilled in the art would readily understand this technique of delivering DNA to a host cell by such means. Although the
15 invention preferably includes adenovirus, the invention is intended to include any virus which serves equivalent functions.

In another preferred embodiment of the present invention, RNA is delivered to competent host cells by means of a retrovirus. One skilled in the art would readily understand this technique of delivering RNA to a host cell by such means. Any retrovirus
20 which serves to express the protein encoded by the RNA is intended to be included in the present invention.

In another preferred embodiment of the present invention, nucleic acid is delivered through folate receptor means. The nucleic acid sequence to be delivered to a host cell is linked to polylysine and the complex is delivered to the tumor cell by means of the
25 folate receptor. U.S. Patent 5,108,921 issued April 28, 1992 to Low *et al.*, which is incorporated herein by reference, describes such delivery components.

The present invention is also related to purified attenuated, non-functional *vif* proteins. The *vif* proteins of the invention have deletions, additions, point mutation(s), multiple substitutions, or introduction of stop codons to produce peptides that are attenuated
30 and non-functional compared to wild type *vif* protein. In preferred embodiments of the invention, the attenuated, non-functional *vif* proteins of the invention comprise an amino acid

sequence selected from the group consisting of SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22 and SEQ ID NO:23. In other preferred embodiments of the invention, the attenuated, non-functional *vif* proteins of the invention consist of an amino acid sequence selected from the group consisting of SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22 and SEQ ID NO:23. The *vif* proteins of the invention may be prepared by routine means using readily available starting materials as described above.

The particulars for the construction of expression systems suitable for desired hosts are known to those in the art and are described above. For recombinant production of the protein, the DNA encoding it is suitably ligated into the expression vector of choice and then used to transform the compatible host which is then cultured and maintained under conditions wherein expression of the foreign gene takes place. The proteins of the present invention thus produced are recovered from the culture, either by lysing the cells or from the culture medium as appropriate and known to those in the art. One having ordinary skill in the art can, using well known techniques, isolate an attenuated, non-functional *vif* protein that is produced using such expression systems. Methods of purifying an attenuated, non-functional *vif* protein from natural sources using antibodies which specifically bind to an attenuated, non-functional *vif* protein may be equally applied to purifying an attenuated, non-functional *vif* protein produced by recombinant DNA methodology.

In addition to producing these proteins by recombinant techniques, automated amino acid synthesizers may also be employed to produce *vpr* protein. It should be further noted that if the proteins herein are made synthetically, substitution by amino acids which are not encoded by the gene may also be made. Alternative residues include, for example, the ω amino acids of the formula $H_2N(CH_2)_nCOOH$ wherein n is 2-6. These are neutral, nonpolar amino acids, as are sarcosine (Sar), t-butylalanine (t-BuAla), t-butylglycine (t-BuGly), N-methyl isoleucine (N-Melle), and norleucine (Nleu). Phenylglycine, for example, can be

substituted for Trp, Tyr or Phe, an aromatic neutral amino acid; citrulline (Cit) and methionine sulfoxide (MSO) are polar but neutral, cyclohexyl alanine (Cha) is neutral and nonpolar, cysteic acid (Cya) is acidic, and ornithine (Orn) is basic. The conformation conferring properties of the proline residues may be obtained if one or more of these is substituted by hydroxyproline (Hyp).

Pharmaceutical compositions according to the invention comprise a pharmaceutically acceptable carrier in combination with either an attenuated, non-functional *vif* protein or a nucleic acid molecule of the invention encoding the same. In preferred embodiments of the invention, the pharmaceutical composition comprises a recombinant expression vector that encodes a *vif* protein comprising the amino acid sequence selected from the group consisting of SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22 and SEQ ID NO:23.

In other preferred embodiments of the invention, the pharmaceutical composition comprises a nucleic acid molecule encoding a *vif* protein which comprises a nucleotide sequence selected from the group consisting of SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45 and SEQ ID NO:46. Pharmaceutical formulations are well known and pharmaceutical compositions comprising the compounds of the invention may be routinely formulated by one having ordinary skill in the art. Suitable pharmaceutical carriers are described in *Remington's Pharmaceutical Sciences*, A. Osol, a standard reference text in this field, which is incorporated herein by reference in its entirety.

The present invention also relates to an injectable pharmaceutical composition that comprises a pharmaceutically acceptable carrier and a compound of the present invention. The compound of the invention is preferably sterile and combined with a sterile pharmaceutical carrier. In some embodiments, for example, the compounds of the invention can be formulated as a solution, suspension, emulsion or lyophilized powder in association with a pharmaceutically acceptable vehicle. Examples of such vehicles are water, saline,

Ringer's solution, dextrose solution, and 5% human serum albumin. Liposomes and nonaqueous vehicles such as fixed oils may also be used. The vehicle or lyophilized powder may contain additives that maintain isotonicity (e.g., sodium chloride, mannitol) and chemical stability (e.g., buffers and preservatives). The formulation is sterilized by commonly used techniques.

An injectable composition may comprise a compound of the invention in a diluting agent such as, for example, sterile water, electrolytes/dextrose, fatty oils of vegetable origin, fatty esters, or polyols, such as propylene glycol and polyethylene glycol. The injectable must be sterile and free of pyrogens.

Formulations for topical administration may include transdermal patches, ointments, lotions, creams, gels, drops, suppositories, sprays, liquids and powders. Conventional pharmaceutical carriers, aqueous, powder or oily bases, thickeners and the like may be necessary or desirable. Compositions for oral administration include powders or granules, suspensions or solutions in water or non-aqueous media, capsules, sachets or tablets. Thickeners, flavoring agents, diluents, emulsifiers, dispersing aids or binders may be desirable. Compositions for parenteral, intrathecal or intraventricular administration may include sterile aqueous solutions which may also contain buffers, diluents and other suitable additives.

The pharmaceutical compositions of the present invention may be administered by any means that enables the active agent to reach the agent's site of action in the body of a mammal. The pharmaceutical compositions of the present invention may be administered in a number of ways depending upon whether local or systemic treatment is desired and upon the area to be treated. Administration may be topical (including ophthalmic, vaginal, rectal, intranasal, transdermal), oral or parenteral. Parenteral administration includes intravenous drip, subcutaneous, intraperitoneal or intramuscular injection, pulmonary administration, e.g., by inhalation or insufflation, or intrathecal or intraventricular administration.

Dosage varies depending upon known factors such as the pharmacodynamic characteristics of the particular agent, and its mode and route of administration; age, health, and weight of the recipient; nature and extent of symptoms, kind of concurrent treatment, frequency of treatment, and the effect desired. Formulation of therapeutic compositions and their subsequent administration is believed to be within the skill of those in the art.

According to the invention, the pharmaceutical composition comprising a nucleic acid molecule that encodes a *vif* protein of the invention may be administered directly into the individual or delivered *ex vivo* into removed cells of the individual which are reimplanted after administration. By either route, the genetic material is introduced into cells which are present in the body of the individual. Preferred routes of administration include intramuscular, intraperitoneal, intradermal and subcutaneous injection. Alternatively, the pharmaceutical composition may be introduced by various means into cells that are removed from the individual. Such means include, for example, transfection, electroporation and microprojectile bombardment. After the nucleic acid molecule is taken up by the cells, they are reimplanted into the individual.

The pharmaceutical compositions according to this aspect of the present invention comprise about 0.1 to about 1000 micrograms of DNA. In some preferred embodiments, the pharmaceutical compositions contain about 1 to about 500 micrograms of DNA. In some preferred embodiments, the pharmaceutical compositions contain about 25 to about 250 micrograms of DNA. Most preferably, the pharmaceutical compositions contain about 100 micrograms DNA.

The pharmaceutical compositions according to this aspect of the present invention are formulated according to the mode of administration to be used. One having ordinary skill in the art can readily formulate a nucleic acid molecule that encodes a *vif* protein of the invention. In cases where intramuscular injection is the chosen mode of administration, an isotonic formulation is used. Generally, additives for isotonicity can include sodium chloride, dextrose, mannitol, sorbitol and lactose. Isotonic solutions such as phosphate buffered saline may be used. Stabilizers include gelatin and albumin.

DNA-based pharmaceutical agents are being developed as a new generation of vaccines. DNA therapeutics are typically plasmids that contain one or more DNA vaccines are typically plasmids which contain one or more genes from a particular pathogen or undesirable cell. Once injected, the coding sequence of the DNA vaccine is expressed in the patient or vaccinee as protein products and an immune response against the protein product is induced. Examples of protocols for delivering DNA which can be adapted for use with the present invention are described in U.S. Patent No. 5,593,972 issued January 14, 1997 to Weiner, U.S. Patent No. 5,589,466 issued December 14, 1996 to Felgner et al., U.S. Patent

Number 4,945,050 issued July 31, 1990 to Sanford et al., U.S. Patent Number 5,036,006 issued July 30, 1991 to Sanford et al., PCT publication serial number WO 90/11092, PCT publication serial number WO 93/17706, PCT publication serial number WO 93/23552, and PCT publication serial number WO 94/16737 which are each incorporated herein by
5 reference.

In preferred embodiments of the invention, pharmaceutical compositions comprising nucleic acid molecule comprising a nucleotide sequence encoding an attenuated, non-functional *vif* protein is administered to a mammal by the methods described above in order to induce a humoral and/or a cellular immune response to *vif* protein. In other
10 embodiments of the invention, the pharmaceutical compositions of the invention can be co-administered with additional compounds. Such additional compounds include, for example, different viral proteins or nucleic acid molecules encoding a different viral proteins. The different viral proteins include, for example, *gag*, *pol*, *env*, *vpr*, *vpu*, and *tat*, and the like. Such elicited immune responses are protective against HIV or related animal viruses.

The present invention is also directed to antibodies directed against an attenuated, non-functional *vif* protein. As used herein, the term "antibody" is meant to refer to complete, intact antibodies, and Fab fragments and F(ab)₂ fragments thereof. Complete, intact antibodies include monoclonal antibodies such as murine monoclonal antibodies, chimeric antibodies and humanized antibodies. In some embodiments, the antibodies
20 specifically bind to an epitope of *vif* or attenuated, non-functional *vif*. Antibodies that bind to an epitope are useful to isolate and purify that protein from both natural sources or recombinant expression systems using well known techniques such as affinity chromatography. Such antibodies are useful to detect the presence of such protein in a sample and to determine if cells are expressing the protein.

Hybridomas which produce antibodies that bind to *vif* protein, and the antibodies themselves, are useful in the isolation and purification of *vif* and attenuated, non-functional *vif* and protein complexes that include *vif* or attenuated, non-functional *vif*. In addition, antibodies may be specific inhibitors of *vif* activity. Antibodies which specifically bind to *vif* or attenuated, non-functional *vif* may be used to purify the protein from natural
30 sources using well known techniques and readily available starting materials. Such antibodies

may also be used to purify the protein from material present when producing the protein by recombinant DNA methodology.

The production of antibodies and the protein structures of complete, intact antibodies, Fab fragments and F(ab)₂ fragments and the organization of the genetic sequences that encode such molecules are well known and are described, for example, in Harlow, E. and D. Lane (1988) *ANTIBODIES: A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, which is incorporated herein by reference. Briefly, for example, *vif* or attenuated, non-functional *vif*, or an immunogenic fragment thereof, is injected into mice. The spleen of the mouse is removed, the spleen cells are isolated and fused with immortalized mouse cells. The hybrid cells, or hybridomas, are cultured and those cells which secrete antibodies are selected. The antibodies are analyzed and, if found to specifically bind to *vif* or attenuated, non-functional *vif*, the hybridoma which produces them is cultured to produce a continuous supply of antibodies.

The present invention is further illustrated by the following examples, which are not intended to be limiting in any way. All references cited in the present application are incorporated in their entirety.

EXAMPLES

Example 1: Patients

Virus from one HIV-1 positive transmitter mother (T1) and one HIV-1 positive non-transmitter mother (N1) were used in the present invention. Peripheral blood lymphocytes (PBLs) obtained during the subject's third trimester were provided by the Mother Infant Cohort Study, Viral Epidemiology Branch, NCI (Rockville, MD). A follow up examination was performed on the subjects and their offspring in order to determine transmission status.

25 Example 2: HIV-1 Isolation

Infected primary lymphocytes were co-cultivated with PHA-stimulated normal donor lymphocytes for 2 weeks. Virus production was monitored by: 1) measuring the levels of intracellular HIV-1 reverse transcriptase (RT) (Velpandi, *et al.*, *J. Virol. Meth.*, **1990**, 29, 291; incorporated herein by reference) and 2) measuring the amount of HIV-1 p24 antigen

released into the medium using a p24 antigen kit (Coulter Corporation), used according to the manufacturer's guidelines.

Example 3: DNA Preparation And PCR Amplification

High molecular weight (genomic) DNA was prepared from the infected PBLs and amplifies through PCR technology as described in Velpandi, *et al.*, *J. Virol. Meth.*, **1990**, 29, 291, incorporated herein by reference. Briefly, the PCR mixture contained 5 to 10 µg of genomic DNA, 50 mM KCl, 2.5 mM MgCl₂, 10 mM Tris/HCl (pH 8.0), 800 µM dNTPs, 2.5 units Taq polymerase, 20 pmol oligonucleotide primers and double de-ionized water (ddH₂O) in a final volume of 100 µl. Reaction temperatures and cycling times were: 94°C-denaturing (1 minute), 55°C-annealing (1.5 minutes) and 72°C-extension (2 minutes). The cycle was repeated 35 times. The primer sequences are as follows: Vif(+) 5'-GAAAGCTTATGGAAAACAGATGGCAG-3' (5046-5065) (SEQ ID NO:2); and Vif(-) 5'-GCAAAGCTTTCATTGTATGGCTC-3' (5609-5626) (SEQ ID NO:3). The primers were tagged with a HindIII restriction site (in bold) for cloning purposes.

15 Example 4: Cloning And Sequencing

PCR-amplified product was used for cloning as described in Velpandi, *et al.*, *DNA Cell Biol.*, **1996**, 15, 571, incorporated herein by reference. Plasmid DNA positive for the *vif* gene was purified by mini preparations (Qiagen, CA) and quantitated by spectrophotometry in preparation for sequencing of the insert. Sequencing reactions were performed using an ABT automated sequencer and Dye Deoxy reactions (Applied Biosystems, Foster City, CA).

Example 5: Sequence Analysis

Sequence alignments were constructed using the Genetics Computer Group Sequence Analysis software package acquired through the Medical School Computer Facility of the University of Pennsylvania VAX system. Homology comparisons of amino acid sequences were carried out by sequence alignment programs.

Example 6: Construction Of Vif-Defective Provirus

HIV-1 proviral DNA, pZr6, was used to construct a vif deletion mutant as described in Nagashunmugam, *et al.*, *DNA Cell Biol.*, **1996**, *15*, 353, incorporated herein by reference. The resulting proviral clone, p911, contains an 80 amino acid deletion in the vif gene which does not affect the 3' reading frame. Briefly, HIV-1 proviral DNA pZr6 was derived from primary blood lymphocytes infected with HIV_{Z6} as described in Srinivasan, *et al.*, *Gene*, **1987**, *52*, 71-82, incorporated herein by reference in its entirety. A deletion was introduced into pZr6 to prepare p911. The mutant was constructed so as not to interfere with the upstream *pol* gene or the downstream *vpr* gene. Plasmid pZr6 contains two *NdeI* sites in the vif gene at nucleotide positions 476 and 716. Srinivasan, *et al.*, *Gene*, **1987**, *52*, 71-82. The *NdeI* fragment (477-716) was deleted from pZr6 and the ends were religated to construct p911, an in-frame mutant that has 80 amino acids deleted in the central region of the vif protein.

Example 7: Construction Of Vif Expression Vectors

The vif expression plasmid, pCVif, contains the vif gene from the well-characterized HIV-1 molecular clone, pHXB2, under the control of the cytomegalovirus (CMV) immediate early promoter, within the backbone plasmid, pRc/CMV (Invitrogen, San Diego, CA) as described in Nagashunmugam, *et al.*, *DNA Cell Biol.*, **1996**, *15*, 353, incorporated herein by reference. The vif genes from the maternal samples were cloned into the Invitrogen expression vector, pCDNA3, under the control of the CMV promoter. The vif reading frames were verified through sequence analysis using the forward primer, T7, and the reverse primer, SP6. Briefly, to construct a vif expression vector (pCVif), an *EcoRI-EcoRI* 1.1 kb fragment from pHXB2 (map coordinates 4,647-5,742; Ratner, *et al.*, *Nature*, **1985**, *313*, 277-284, incorporated herein by reference in its entirety) was cloned under the control of the cytomegalovirus immediate early promoter into plasmid pCDNA3 obtained from Invitrogen. This fragment also contains flanking sequences from parts of the *pol* and *vpr* genes, which are not transcriptionally active as shown in a similar construct by Blanc, *et al.* (*Virology*, **1993**, *193*, 186-192).

Example 8: In Vitro Translation Of Vif

In vitro transcription and translation was performed on 1 µg of *vif* expression construct DNA using T7 RNA polymerase according to the manufacturer's instructions (Promega, Madison, WI). Five (5) µl of the *in vitro* translation reaction products were combined with 500 µl of radioimmunoprecipitation assay buffer and immunoprecipitated with rabbit anti-vif antiserum as described. Mahalingam, *et al.*, *Virology*, **1995**, 214, 647.

Example 9: Cells

Rhabdomyosarcoma (RD) cells, obtained from the American Type Culture Collection (ATCC), were grown in a monolayer at 37°C in 5% CO₂ in Dulbecco's modified Eagle's medium supplemented with 10% fetal bovine serum, 1% penicillin, 1% streptomycin and 1% L-glutamine. Lymphocytoid cell lines obtained from ATCC were maintained as suspension cultures in RPMI 1640 medium, supplemented with 10% fetal bovine serum, penicillin (100 U/ml) and L-glutamine (540 µg/ml) at 37°C with 5% CO₂. Phytohemagglutinin-stimulated (10 µg/ml) PBLs were maintained in RPMI 1640 medium containing 10% T-cell growth factor.

Example 10: Immunization Of Mice With Vif Constructs

For immunization experiments in mice, 3 different *vif* constructs were used. The *vif* clones selected were T-35 (from transmitter), N-15 (from non-transmitter) and pCVif (*vif* gene of HIV-1_{SP-2}). pCDNA3 vector DNA was used as a negative control. In order to enhance DNA uptake, the quadriceps muscles of BALB/c mice were injected with 100 µl of 0.25% bupivacaine 48 hours before DNA injection. Fifty (50) or 100 µg of each *vif* expression plasmid was injected in a final volume of 100 µl into each of 4 mice. The animals were boosted 3 times at two week intervals.

Example 11: ELISA Binding Of Mouse Serum To rvif Protein

ELISA was performed on mouse serum as described in Wang, *et al.*, *AIDS*, **1995**, 9 (Suppl A), S159. Briefly, ELISA plates were coated with recombinant vif (rvif) protein at concentration of 100 ng/well for the binding assays. Mouse sera were diluted (1:100 and 1:500) in blocking buffer, tagged with anti-mouse IgG conjugated to horseradish

peroxidase (HRP) and detected by TMBBlue substrate. The non-specific binding and the prebled sera binding were subtracted from the specific binding of the DNA injected animal sera.

Example 12: CTL Assay Using Vaccinia Expressing *vif*

- 5 DNA injected mice were sacrificed 7 weeks after the first immunization, and their spleens were removed for CTL and T-cell proliferation assays as described in Wang, *et al.*, *DNA Cell Biol.*, **1993**, *12*, 799. Briefly, P815 cells infected with *vif*-expressing vaccinia (VV:gag kindly provided by NIH AIDS Reagent and Reference Program) were used as target cells. Ten (10) μCi of Na_2CrO_4 (^{51}Cr , 534 mCi/mg, Dupont Co.) was added to $1 \times 10^6/\text{ml}$
- 10 target cells which were subsequently incubated for 2 hours at room temperature. The cells were then washed 3 times with serum-free media and diluted to a volume of 1×10^5 cells/ml in RPMI 1640/10% calf serum. The effector spleen cells were washed once, resuspended and diluted to a concentration of 1×10^7 cells/ml of RPMI medium. 1:2 serial dilutions were made from this stock cell solution (5×10^6 , 2.5×10^6 and 1.25×10^6 cells/ml). One hundred (100)
- 15 μl of these effector cell solutions were aliquoted into a 96-well microliter flat bottom plate. One hundred (100) μl of target cell solution was added to each well. The resultant effector to target cell ratios were 100:1, 50:1, 25:1 and 12.5:1. In order to determine the spontaneous or maximum chromium release, respectively, target cells were mixed with either 100 μl of media alone or 1% Triton-X. The effector and target cells were then incubated at 37°C in a
- 20 5% CO_2 incubator for 5 hours. A 100 μl aliquot of supernatant was removed from each well, and the amount of ^{51}Cr release was measured in a gamma counter. The formula for calculation of the specific CTL release is below: $100 \times [(\text{experimental release} - \text{spontaneous release}) / (\text{maximum release} - \text{spontaneous release})]$. Note: maximum release was determined by lysis of target cells in 1% Triton X-100.

25 Example 13: CTL Assay Using Clinical HIV-1 Isolates

HeLa CD4+ cells expressing mouse MHC-I were infected with HIV-1 clinical isolates and used as target cells in the CTL assay. The CTL assay was performed as described in Chada, *et al.*, *J. Virol.*, **1993**, *67*, 3409.

Example 14: T Cell Proliferation Assay

Assays were performed in triplicate. Splenocytes were isolated as discussed above, resuspended in RPMI 1640 and diluted to a concentration of 3.3×10^6 cells/ml. A 150 μ l aliquot was immediately added to each well of a 96-well microtiter flat bottom plate.

5 Fifty (50) μ l of protein or peptide was added to each well to final concentrations of 10.0, 1.0 or 0.1 mg/ml. The cells were incubated at 37°C in a 5% CO₂ incubator for 3 days. One (1) μ Ci of tritiated thymidine was added to each well, and the cells were incubated overnight under the same conditions. The cells were harvested using automated cell harvester (Tomtec, Orange, CT) and the amount of incorporated tritiated thymidine was measured in a beta

10 counter. In order to ensure that the cells were healthy, 5 mg/ml of PHA was used as a non-specific stimulator in a positive control sample.

Example 15: Transcomplementation Of vif Defective Proviral DNA With vif Genes From Maternal Samples

RD cells (1×10^6) were co-transfected with 10 μ g of a vif defective proviral clone, p911, and 10 μ g pCVif or vif expression plasmid from transmitter or non-transmitter subjects using lipofectin from Boehringer Mannheim (Indianapolis, IN). The co-transfected cells were washed after an 8 hour incubation and resuspended in DMEM media. Culture supernatant was collected after a 72 hour incubation, centrifuged to remove cell debris, passed through a 0.45 μ m filter, and assayed for p24 production (Coulter Corporation). PBMCs (1

15 $\times 10^7$) were infected with an amount of virus equivalent to 100 ng of p24 antigen. Virus-inoculated cells were incubated for 4-6 hours at 37°C and 5% CO₂, washed 3 times with PBS and resuspended in 10 ml of fresh RPMI 1640. An aliquot of the culture supernatant was collected every 3 days in order to quantitate virus production by measuring the amount of p24 antigen released into the medium.

Example 16: Characterization Of Viruses Isolated From Patients

The HIV-1 positive transmitter and non-transmitter mothers included in the present invention were selected from an AIDS cohort study. The mother and the non-transmitter mother are referred to as T1 and N1, respectively. The clinical status of the subjects and the replication kinetics of their viral isolates are presented in Table 2.

Uncultured lymphocytes from each subject were used in order to obtain wild-type sequences unmodified by *in vitro* selection conditions. In PBMC co-cultivation assays, T1 viral samples replicated very well in normal donor PBLs; whereas N1 viral samples did not replicate in either primary lymphocytes or macrophages.

5

Table 2

Subject	Clinical Stage	PCR	Virus Coculture in PBMC	Infection in CD4+ Cell Lines
Transmitter	Asymptomatic	+++	+++	+++
Non-Transmitter	Asymptomatic	++	---	---

Example 17: Sequence Variation Of *Vif* Gene In Vivo

10

In order to investigate the genetic variability of the *vif* gene in these subjects, ten clones from each subject were sequenced and computer-aligned by degree of homology. The nucleotide sequences were then translated into protein sequences. Deduced amino acid sequences were used in the final comparison, since not all nucleotide sequence changes resulted in amino acid sequence changes. The aligned amino acid sequences from these

15

patients are shown in Figure 1. Clone numbers with the designations, 'T' and 'N' represent variants isolated from transmitter and non-transmitter mothers, respectively. Sequence alignment revealed that each subject had a unique and highly conserved set of sequences within their virus pool. Most of the nucleotide changes were point mutations which generally resulted in substitutions, versus duplications or insertions, within the protein sequence. Three

20

clones encoded attenuated proteins. Clone T-42 had a 5 amino acid deletion at its 3' end due to a premature stop codon. Clone N-13 had two stop codons (positions 31 and 41) and clone T-4 had a single stop codon (position 77), each of which was introduced within a set of three nucleotides, keeping the reading frame intact 3' to the mutation. The fact that the majority (17 of 20) of the clones encode full-length sequences suggests that there are few defective *vif*

25

genes present within these patients' viral pools. It is interesting to note that most of the *vif* point mutations are present in the 5' portion of the gene rather than in the 3' region.

Significant differences were found between clones at positions 20, 27, 31, 36, 37, 45, 60, 74, 127, 136, 140 and 150.

In order to determine the nature and the sequence variation of *vif* gene *in vivo*, we cloned and analyzed *vif* variants present in uncultured PBMCs from HIV-1 positive subjects. Analysis of 20 different *vif* sequences from two subjects (10 from each subject) revealed that *vif* is highly conserved (approximately 90%) within a particular patient at a given time point. Although, Wieland, et al. (*Virol.*, **1994**, 203, 43) reported that the 3' portion of the *vif* gene is highly variable, the results of the present invention indicate that the 5' portion (aa 20-85) is more variable and the 3' portion is well-conserved. In support of the results herein, previous mutagenesis experiments have shown that the C terminus of *vif* (aa 171 to 192) is essential for stable association of *vif* with membranes. Goncalves, et al., *J. Virol.*, **1994**, 68, 704. Among the 20 sequences we analyzed, only two clones had premature stop codons indicating that 90% of *vif* genes isolated were intact *in vivo*. This result, along with previously published data, suggests that a complete *vif* gene is essential for viral replication *in vivo*. Gabudza, et al., *J. Virol.*, **1992**, 66, 6489; and Sova, et al., *J. Virol.*, **1995**, 69, 2557.

The 20 deduced *vif* protein sequences from these clones exhibited 75% conservation (25% variation) over the entire (192 aa) length. In particular, two antigenic domains, aa 87-94 (IEWRKKRY) (SEQ ID NO: 24) and aa 172-178 (DRWNKPQ) (SEQ ID NO: 25), recognized by HIV-1 positive sera (Wieland, et al., *AIDS Res. Human Retrovir.*, **1991**, 7, 861) are well conserved in all 20 clones. The well-conserved nature of these two regions may be responsible for the cross antigenic properties exhibited by these clones. In addition, a sequence which is conserved in 34/38 lentivirus *vif*, SLQYLA (144-149) (SEQ ID NO: 26) (Oberste, et al., *Virus Genes*, **1992**, 6, 95), is also conserved in each of the 20 *vif* clones sequenced in the present invention. In previous studies, computer alignment analyses has shown that amino acids 21 to 30, 103 to 115 and 142 to 150 of *vif* are highly conserved among HIV-1, HIV-2 and SIV. Myers, et al., *Human Retrovir. AIDS*, **1988**. Clones analyzed in the present invention, however, were generally conserved sequences within aa 103-115 and aa 142-150, but not within aa 21-30. *Vif* protein has been characterized as a cysteine protease with Cys 114 marking its active site and His 48 considered to be important for activity. Guy,

et al., J. Virol., **1991**, *65*, 1325. In the sequences of the present invention, Cys 114, as well as Cys 133 (the only other cystine in vif) and His 48, were well conserved.

Phylogenetic tree analysis (data not shown) found 3 major families within the 20 patient clones. Ninety (90%) percent of N-derived clones formed a family and 80% of T-derived clones formed a family while the remaining clones, N-30, T-3 and T-38, exhibited greater diversity and formed a Separate group (data not shown). When distance comparison was performed, inpatient variation between the transmitter clones was 12%, versus a variation of 10% between non-transmitter clones. The similarity between the subjects' variant clones and the established laboratory molecular clones, HIV_{SF-2}, HIV_{NL4.3} and HIV_{Z66}, was also evaluated. The subject isolates shared a higher degree of homology with other clones within their transmitter status group than with any of the laboratory-maintained viral isolates. Based upon their sequence variation, 4 clones from each patient were selected for preliminary translation/immunization experiments (see below).

Phylogenetic tree analysis also illustrated that, in spite of intra-patient variation, clones from the transmitter and nontransmitter subjects clustered separately. *In vitro* transcription/translation of 8 constructs (four from each subject) resulted in the expression of a 23 KDa protein, except in the case of clone N-13 which has a premature stop codon. This suggests that the various mutations present in these vif constructs did not affect the expression kinetics and stability of the protein.

Example 18: Expression Of Vif Clones

In vitro transcription/translation was performed upon 5 clones from each group in order to assess their levels of vif expression. Results are presented in Fig. 2. The products from the *in vitro* translation reactions were immunoprecipitated with vif antiserum and subjected to gel electrophoresis. pCVif (full length vif from HIV-1 strain SF2) and p911 (*vif* mutant) provirus were used as a positive and negative control, respectively. *In vitro* translation with pCVif and each of the full length *vif* expression plasmids produced a 23 kDa protein; whereas clones p911 and N-13 did not result a protein product of 23 kDa size, probably due to the presence of premature stop codons. Two (2) clones from each subject group were selected for further evaluation, based upon similar serological characteristics (data not shown). The patient clones selected as representatives from each group were T-35 (from

transmitter) and N-15 (from non-transmitter). Each of these clones contain mutations characteristic of their particular group and represent the highest level of diversity within these groups. It is interesting to note that mutations within clone N-15 are dispersed throughout the full length gene; whereas mutations within clone T-35 are clustered at the 5' end of the gene.

Example 19: Induction Of Humoral Responses *In Vivo*

Specific anti-vif immune responses were apparent in sera collected from mice immunized with T-35, N-15 and pCVif expression plasmids, but not in sera from mice immunized by pcDNA3 vector alone. The induction of immune response correlated with DNA injection concentration, as well as the number and time interval between boosts. Sera from 4 mice injected with either 50 or 100 µg of vif/DNA had specific reactivity to vif protein when measured by ELISA (Fig. 3). Induction of the humoral response was dose- and time-dependent. Injection of 50 µg of DNA induced an immune response detectable by ELISA at 15 days following the first injection. This response increased after subsequent boosts, reaching a maximum level 45 days after 2 boosts (Panel A). Injection with 100 µg of DNA induced a response that reached a maximum level only 28 days after a single boost (Panel B). In addition, the antibody response can be elevated 219 days after the three injections with a single boost of DNA (data not shown). The level of antibody response varied between vif clones. Most importantly, the non-transmitter clone, N-15, induced a higher serological response than the transmitter clone, T-38, or pCVif. This suggests that non-transmitter vif is capable of inducing a more efficient B-T helper dependent response than transmitter vif in this strain of mice.

Example 20: Induction Of Cellular Responses *In Vivo* Using Vaccinia Expressing Vif

Four mice, each immunized with one of the vif constructs, were given an additional boost 15 days after first injection. Two mice were subsequently sacrificed and their splenocytes were used in a cytotoxic T cell (CTL) assay. p815 cells infected with vif-expressing vaccinia were used as target cells. Non-specific lysis by splenocytes from vif DNA immunized and naive mice was measured using p815 cells infected with non-vif-expressing vaccinia as target cells. Specific target lysis is presented in Fig. 4. The level of

specific CTL activity varied between the *vif* constructs. Splenocytes from mice immunized with clone pCVif exhibited 45% lysis at a effector:target ratio of 100:1. Clones T-35 and N-15 exhibited 17 and 12% lysis, respectively, at the same ratio. These results clearly demonstrate that *vif* DNA immunization induces specific CTL responses. The differences in the levels of CTL activity induced by *vif* gene inoculation between the various patient clones may be due to mutations within the CTL epitopes expressed by vaccine targets or differences in immune responsiveness in this haplotype.

Example 21: Evaluation Of Cellular Responses *In Vivo* Using Human Targets Infected With A Clinical HIV-1 Isolate

10 In order to evaluate the ability of the *vif* clones to induce lysis of virally infected targets, we used HIV-1 infectable HeLa CD4/D^Δ cells which express both the CD4 receptor and the murine class IH-2D^Δ restriction element, as targets in the CTL assay. These cells were infected with an HIV-1 isolate derived from a symptomatic AIDS patient for 7 days. Figure 5 (A-D) represents CTL assay results. Splenocytes obtained from mice injected with each of the DNA constructs exhibited *vif*-specific lysis. Clones T-35, N-15 and pCVif presented with 27, 26 and 24% lysis, respectively, at an effector:target ratio of 50:1. All three clones exhibited 20% lysis at a ratio of 25:1. This demonstrates that a cellular immune response against native HIV-1 isolates can be generated through genetic vaccination with *vif* expression vectors.

20 Example 22: Induction Of Antigen Specific T-Cell Proliferation

Specific T-cell proliferation responses against HIV-1 *vif* protein were also studied in DNA-immunized animals. Lymphocytes from *vif*-immunized mice demonstrated a significant proliferative response against *rvif* protein. Figure 6 illustrates the proliferation index of different *vif* constructs versus DNA injection concentrations. The results show that the MHC class II-dependent T_H (helper) cell response is dose dependent. For each construct, the stimulation index is almost 2-fold higher in mice injected with 100 μg of *vif* DNA than in mice injected with 50 μg of *vif* DNA. Comparison of the three different *vif* constructs also indicates that, at each injection concentration, clone T-35 induces a higher stimulation index than either N-15 or pCVif.

Example 23: Transcomplementation of HIV-1 Vif- Provirus With Vif Expression Plasmids

As expected, transient transfection of RD cells with HIV-1 (*vif*-) proviral DNA and *vif* expression plasmids did not reveal any differences in virus production between T-derived, N-derived or control plasmids (data not shown). Any differences in *vif* function would be demonstrated at the level of new infection. When rescued virus was used to infect primary lymphocytes, however, a significant difference was observed in virus pathogenesis between T- and N-derived and control plasmids (Table 3). The *vif*-negative proviral clone (p911) alone was unable to infect primary PBLs as cell-free virus. When trans-complemented virus (p911 + pCVif) was used to infect the PBLs, infectivity was five-fold less than that of wild-type virus. In contrast, each of the T-derived clones tested were able to rescue the (*vif*-) mutant (approximately 100% positive virus control). However, none of the N-derived clones were able to efficiently infect PBLs as cell-free virus. Therefore, N-15 and similar N-derived clones were able to induce anti-HIV immune responses in mice in the absence of functionality.

Table 3

Samples	DNA Used to Derive Viruses for Infection	Amount of p24 Released (ng/ml)
Proviral Clone	pZr6	101,846
Vif Mutant	p911	60
Vif Mutant + pCVif	p911 + pCVif	22,679
Vif Mutant + Transmitter Clones	p911 + T1-40	21,896
	p911 + T1-37	17,230
	p911 + T1-35	19,470
	p911 + T1-38	81,570
Vif Mutant + Non- Transmitter Clones	p911 + N1-13	520
	p911 + N1-15	530
	p911 + N1-17	1,090
	p911 + N1-27	1,277
	p911 + N1-30	715

RD cells were transfected with 10 µg of pZr6, vif mutant p911, p911 and vif expression plasmids from different patient samples. Virus pools were prepared from supernatant collected 72 hours after transfection. Virus equivalent to 100 ng of p24 antigen was subsequently used to infect 10×10^6 PBMCs. Infection was monitored by p24 antigen production.

Example 24: Observations

N-derived clones were attenuated in their ability to transcomplement vif defective HIV-1 provirus. One of the clones analyzed, N-15, was also immunologically functional and capable of generating an immune response against wild-type HIV-1 virus. A non-functional yet immunogenic clone, such as N-15 in the present invention, could be an effective component of a genetic vaccine directed against HIV-1. It has been shown in the present invention that vif alone can generate an effective response against native HIV-1 virus *in vitro*. Such immunogens could be useful in a therapeutic setting to target the immune response against native vif expressing viruses. While it is likely that escape variants can occur viruses expressing defective vifs due to this selection might now exhibit attenuated *in vivo* growth kinetics. In a similar manner a prophylactic vaccine which includes vif could serve to both limit viral escape and contribute to lowering the viral set point during the early infection events.

What is Claimed is:

1. An isolated, attenuated, non-functional *vif* protein.
2. The protein of claim 1 wherein said protein comprises an amino acid sequence selected from the group consisting of SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, and SEQ ID NO:23.
3. An isolated nucleic acid molecule comprising a nucleotide sequence encoding an attenuated, non-functional *vif* protein.
4. The nucleic acid molecule of claim 3 wherein said nucleic acid molecule comprises a nucleotide sequence which encodes an amino acid sequence selected from the group consisting of SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22 and SEQ ID NO:23.
5. The nucleic acid molecule of claim 3 wherein said nucleic acid molecule comprises a nucleotide sequence selected from the group consisting of SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45 and SEQ ID NO:46.
6. A pharmaceutical composition comprising a protein of claim 1 in a pharmaceutically acceptable carrier or diluent.

7. A pharmaceutical composition comprising a nucleic acid molecule of claim 3 in a pharmaceutically acceptable carrier or diluent.
8. A recombinant expression vector comprising a nucleic acid molecule of claim 3.
9. The recombinant expression vector of claim 8 wherein said nucleic acid molecule comprises a nucleotide sequence which encodes an amino acid sequence selected from the group consisting of SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22 and SEQ ID NO:23.
10. A host cell comprising a recombinant expression vector comprising a nucleic acid molecule of claim 3.
11. The host cell of claim 8 wherein said nucleic acid molecule comprises a nucleotide sequence which encodes an amino acid sequence selected from the group consisting of SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22 and SEQ ID NO:23.
12. A purified antibody directed against an attenuated, non-functional *vif* protein.
13. The antibody of claim 12 wherein said protein comprises an amino acid sequence selected from the group consisting of SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, and SEQ ID NO:23.

14. A method of immunizing a mammal against a virus comprising administering to cells of said mammal, a nucleic acid molecule that comprises a nucleotide sequence that encodes an attenuated, non-functional *vif* protein, wherein said nucleic acid molecule is expressed in said cells.
15. The method of claim 14 wherein said nucleic acid molecule comprises a nucleotide sequence which encodes an amino acid sequence selected from the group consisting of SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22 and SEQ ID NO:23.
16. The method of claim 14 wherein said nucleic acid molecule comprises a nucleotide sequence selected from the group consisting of SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45 and SEQ ID NO:46.
17. The method of claim 14 wherein said virus is selected from the group consisting of human immunodeficiency virus, feline immunodeficiency virus, bovine immunodeficiency virus, Visna virus, and simian immunodeficiency virus.
18. A plasmid comprising a nucleotide sequence encoding an isolated, attenuated, non-functional *vif* protein.
19. The plasmid of claim 18 wherein said protein comprises an amino acid sequence selected from the group consisting of SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, and SEQ ID NO:23.

20. The plasmid of claim 18 wherein said nucleotide sequence is selected from the group consisting of SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45 and SEQ ID NO:46.

101	151	194
N24	h	h
N27	h	h
N26	h	h
N15	h	h
N17	h	h
N23	h	h
N29	h	h
N28	h	h
N13	h	h
N22	h	h
T39	h	h
T44	h	h
T43	h	h
T37	h	h
T40	h	h
T35	h	h
T4	h	h
T3	h	h
T38	h	h
T42	h	h
Con	h	h

1/17

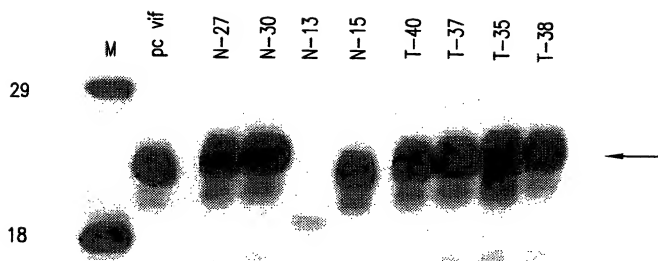


FIG.2

FIGURE 3B

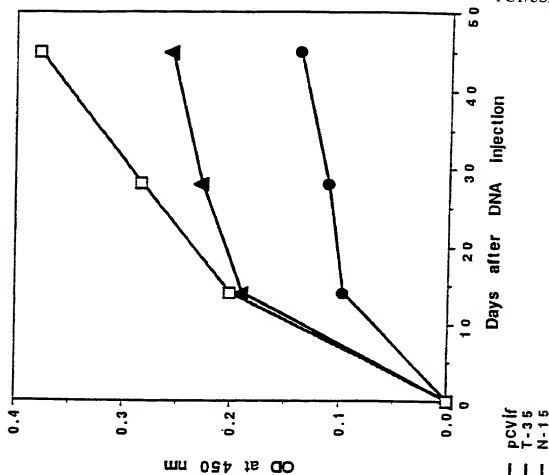
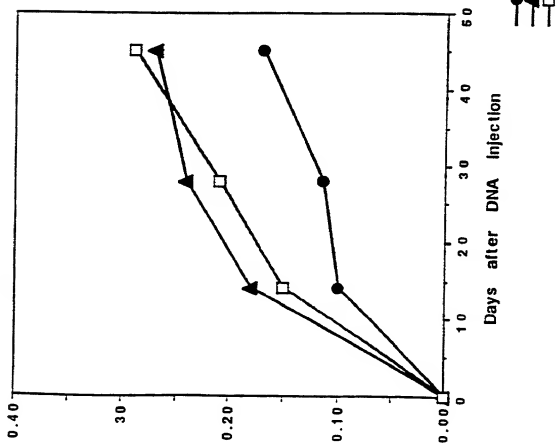


FIGURE 3A



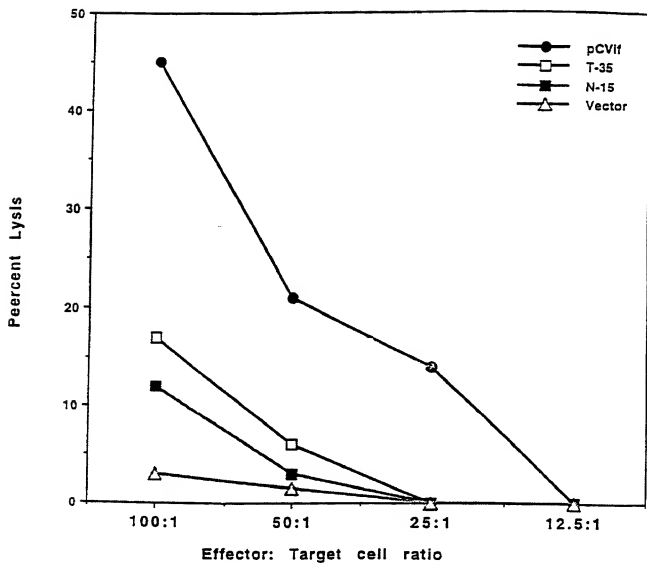


FIGURE 4

FIGURE 5B

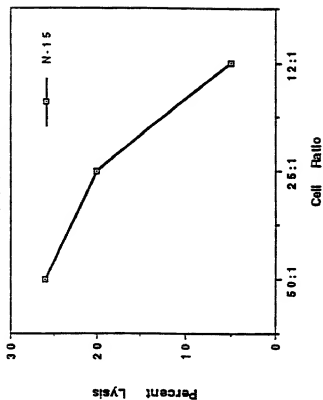


FIGURE 5D

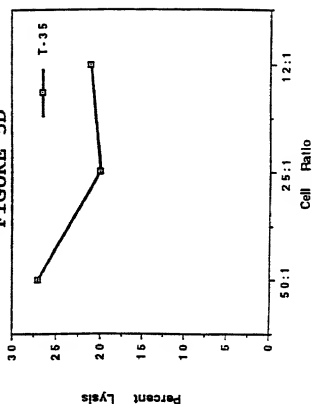


FIGURE 5A

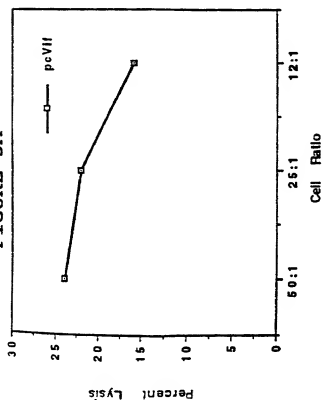
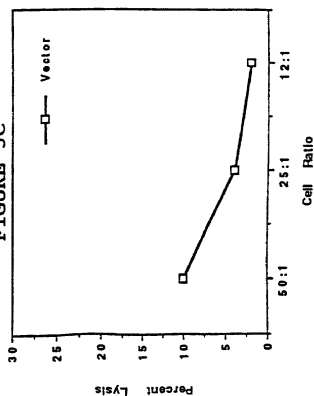
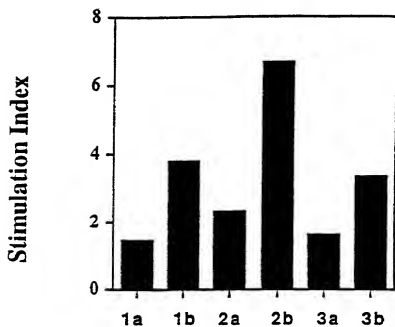


FIGURE 5C



T-cell proliferation



Vif expression constructs used

FIGURE 6

FIGURE 7A

1. vif-N13.pap

MENRWQVIV WQVDRMRIRT WNSLVKYHMY *SKKAREWFY *HHYQSPHPK
 VSSEVHIPLE DARLETTSEW GLHTIGERDAH LGQGVSTEAR KRRYSTHVDP
 DLADQLIHLY YFDCFSESAT RKAILGHRVS PRCEYRAGHS KVGSLQYLAI
 AALITPKKIK PPLASVRKLT EDWANKPQKT KGHGSHIMN GH*

2. Vif-N15.pap

MENRWQVIV WQVDRMRIRT WNSLVKYHMY RSKKAREWFY RHHYQSPHER
 VSSEVHIPLE DARLETTTYW GLHTIGERDAH LGQGVSTEAR KRRYSTQVDP
 DLADQLIHLY YFDCFSESAT RKAILGHRVS PRCEYRAGHS KVGSLQYLAI
 AALITPKKIK PPLPSVRKLT EDWANKPQKT KGHGSHIMN GH*

3. Vif-N17.pap

MENRWQVIV WQVDRMRIRT WNSLVKYHMY RSKKAREWFY RHHYQSPHER
 VSSEVHIPLE DARLETTTYW GLHTIGERDAH LGQGVSTEAR KRRYSTQVDP
 DLADQLIHLY YFDCFSESAT RKAILGHRVS PRCEYRAGHS KVGSLQYLAI
 AALITPKKIK PPLPSVRKLT EDWANKPQKT KGHGSHIMN GH*

FIGURE 7B

4. Vif-N22.pap

MENRWQVMIV WQVDRMRIRT WNSLVYHYMY RSQKAREWFN RHHVHSPHPK
 VSSEVHIPLE DARLAIPTFW GLHTIGERDAH LQQGVSTEAR KRRYSTQVDP
 DLADQLIHLY YFDCFSESAT RKAILGHRVS PRCEYRAGHS KVGSLQYLAI
 AALITPKKIK PPLPSVRKLT EDRWNPQKT KHRGSHIMN GH*

5. Vif-N24.Pap

MENRWQVMIV WQVDRMRIRT WNSLVKYHYMY RSKKAREWFY RHHYQSPHPK
 VSSEVHIPLE DARLVITTYW GLHTIGERDAH LQQGVSTEAR KRRYSTHVDP
 DLADQLIHLY YFDCFSESAT RKAILGHRVS PRCEYRAGHS KVGSLQYLAI
 AALITPKKIK PPLASVRKLT EDRWNPQKT KHRGSHIMN GH*

6. Vif-N26.pap

MENRWQVMIV WQVDRMRIRT WNSLVKYHYMY RSKKAREWFY RHHYQSPHPK
 VSSEVHIPLE DARLVITTYW GLHTIGERDAH LQQGVSTEAR KRRYSTHVDP
 DLADQLIHLY YFDCFSESAT RKAILGHRVS PRCEYRAGHS KVGSLQYLAI
 AALITPKKIK PPLASVRKLT EDRWNPQKT KHRGSHIMN GH*

7. Vif-N27.pap

MENRWQVMIV WQVDRMRIRT WNSLVKYHYMY RSKKAREWFY RHHYQSPHPK
 VSSEVHIPLE DARLVITTFW GLHTIGERDAH LQQGVSTEAR KRRYSTHVDP
 DLADQLIHLY YFDCFSESAT RKAILGHRVS PRCEYRAGHS KVGSLQYLAI

FIGURE 7C

AALITPKKIK PPLPSVRKLT EDWANKPQKT KHRGSHIMN GH*

8. Vif-N29.pap

MENRWQVMIV WQVDRMRIRT WNSLVKYHMY RSKKAREWEN RHHYHRPHPK
 VSSEVHIPLD DARLETTTFW GLHTGERDAW LQGVSTIEWR KRRYSTQVDP
 DLADQLIHLY YFDCFSesai RKAILGHRVS PRCEYRAGHS KVGSLQYLAI
 AALITPKKIK PPLPSVRKLT EDWANKPQKT KHRGSHIMN GH*

9. Vif-N30.

MENRWQVMIV WQVDRMRIRT WNSLVKYHMY RSQKEREWEN RHHYHSPHPE
 QSSTAHIFLV DGRLEKIAW SLDTGEGVAH RGRVSTIEWR KRRYSTQVDP
 DLVDQLIHLY YFDCFSesai RKAILGHRVS PRCEYRAGHS KVGSLQYLAI
 AALITPKKIK PPLPSVRKLT EDWANKPQKT KHRGSHIMN GH*

Vif-T3.pap

MENRWQVMIV WQVDRMRIRT WNSLVKHHMY VSKKAKKWFY RHHYESPHPK
 VSSTAHIFLG DGRLEKTAW SLQAGDGVWH RGHVSTIEWR KRRYSTQVDP
 DLVDQLIHLY YFDCFSesai RKAILGYRVS PRCEYQAGHN KVGSLQYLAI
 AALITPKKIK PPLPSVRKLT EDWANKPQKT KHRGSHIMN GH*

Vif-T35.pap

FIGURE 7D

MENRWQVMIV WQVDRMRIRA WNSLVKHHIY FSKKAKKWFY RHHYESPHFN
 VSSEVHIPLG DARLVITPYW GLHGERDWH LAQGVSTIWR KRRYSTQVDP
 DLADQLIHLY YFDCFSESAI RKAILGYRVS PRCEYQAGHN KVGSLQVLAL
 AALITPKKIK PPLPSVRKLT EDRWKPQKT KHRGSHIMN GH*

Vif-T37.pap

MENRWQVMIV WEVDRMRIRA WNSLVKHHMY VSKKAKKWFY RHHYESPHFK
 VSSEVHIPLG DARLVITPYW GLHGERDWH LQGVSTIWR KRRYSTQVDP
 DLADQLIHLY YFDCFSESAI RKAILGYRVS PRCEYQAGHN KVGSLQVLAL
 AALITPKKIK PPLPSVRKLT EDRWKPQKT KHRGSHIMN GH*

Vif-T38.pap

MENRWQVMIV WQVDRMRIRA WNSLVKHHMY VSKNAKWFY RHHYDSHPK
 QSSIAHIPLG DGRLOKIAFW SLDAGERDWH LQGVSTIWR KRRYSTQVDP
 DLADQLIHLY YFDCFSESAI RKAILGYRVS PRCEYQAGHN KVGSLQVLAL
 AALITPKKIK PPLPSVRKLT EDRWKPQKT KHRGRHIMN GH*

Vif-T39.pap

MENRWQVMIV WQVDRMRIRA WNSLVKHHMY VSKKAKKWFY RHHYDSHPK
 VSSEVHIPLG DARLEITPYW GLHGERDWH LQGVSTIWR KRRYSTHVP

FIGURE 7E

DLADQLIHLV YFDCFSESAI RKAILGYRVS PRCEYQAGHN KVGSLQYLAL
AALITPKKIK PPLPSVRKLT EDRWNPQKT KGHGSHIMN GH*

Vif-T4.pap

MENRWQVMIV WQVDRMTIRA WNSLVKHHMY VSKKARIWFS RHHYGSPPHK
VCSEVHIPLG DARLVITITYW SLHAGE*DAH VGQRVSIEMR KRRYSTQVDP
DLADQLIHLV YFDCFSESAI RKAILGYRVS PRCEYQAGHN KVGSLQYLAL
AALITPKKIK PPLPSVRKLT EDRWNPQKT KGHGSHIMN GH*

Vif-T40.pap

MENRWQVMIV WQVDRMTIRA WNSLVKHHMY VSKKAKKWFY RHHYESPPHK
VSSEVHIPLG DARLVITITYW GLHAGERDWH LGQGVSIEMR KRRYSTQVDP
DLADQLIHLV YFDCFSESAI RKAILGYRVS PRCEYQAGHN KVGSLQYLAL
AALITPKKIK PPLPSVRKLT EDRWNPQKT KGHGSHIMN GH*

Vif-T42.pap

MENRWQVMIV WQVDRMTIRA WNSLVKHHMY VSKKAKKWFN RHHYDRPHK
VSSEVHIPLG DARLETTTFW GLHAGERDWH LGQGVSIEMR KRRYSTQVDP
DLADQLIHLV YFDCFSESAI RKAILGYRVS PRCEYQAGHN KVGSLQYLAL
AALITPKKIK PPLPSVRKLT EDRWNPQKT KGTECAIQ*

FIGURE 7F

Vif-T43.pap

MENRWQVMIV WQVDRMRIRA WNSLVKHHMF VSKKAKWIFY RHYESPHPK
 VSSEVHIPLG DARLEITTFW GLHAGERDWH LGQGVSIENR KRRYSTQVDP
 DLADQLIHLY YFGCFSESAI RKAILGYRVS PRCEYQAGHN KVGSLQYLGL
 AALITPKKIK PPLPSVRKLT EDRANKPKKT KHRGSHIMN GH*

Vif-T44.pap

MENRWQVMIV WQVDRMRIRA WNSLVKHHMY VSKKAKWIFY RHYESPHPK
 VSSEVHIPLG DARLEITTFW GLHAGERDWH LGQGVSIENR KRRYSTQVDP
 DLADQLIHLY YFGCFSESAI RKAILGYRVS PRCEYQAGHN KVGSLQYLAL
 AALITPKKIK PPLPSVRKLT EDRANKPKKT KHRGSHIMN GH*

FIGURE 8A

N13 (SEQ ID NO:27)

ATGGAAACAGATGGCAGGTGATTATTGTGTGGCAGGTAGACAGGATGAGGATTAGAACA
TGGAACAGTTTAGTAAAAATACCATATGTATAGATCAAAGAAAGCTAGGGAAATGGTTTTAT
TGACATCACTATCAAAGTCCTCATCCAAAAGTAAGTTCAGAAGTACACATCCCCTAGAG
GATGCTAGATTGGAATAACATCATTTTGGGGTCTGCATACAGGAGAAAGAGACTGGCAT
TTGGGTCAGGGAGTCTCCATAGAATGGAGGAAAAGGAGATATAGCACACACGTCGACCT
GATCTAGCAGACCAACTAATTATCTGTATTATTGATTGTTTTTTCAGAAATCTGCTATA
AGAAAAGCCATATTAGGACACAGAGTTAGTCTTAGGTTGTAATATCGAGCAGGCATAGC
AAGGTAGGATCACTACAGTACTTGGCAATAGCAGCATTATTAACACCAAAAAGATAAAG
CCACCTTTGGCGAGTGTGAGGAACTGACAGAGGATAGATGGAACAAGCCCCAGAAGACC
AAGGGCCACAGAGGGAGCCATACAATGAATGGACACTAG

N15 (SEQ ID NO:28)

ATGGAAACAGATGGCAGGTGATGATTGTGTGGCAGGTAGACAGGATGAGGATTAGAACA
TGGAACAGTTTAGTAAAAATACCATATGTATAGATCAAAGAAAGCTAGGGAAATGGTTTTAT
AGACATCACTATCAAAGTCCTCATCCAAGAGTAAGTTCAGAAGTACACATCCCCTAGAG
GATGCTAGATTGGAATAACACATATTGGGGTCTGCATACAGGAGAAAGAGACTGGCAT
TTGGGTCAGGGAGTCTCCATAGAATGGAGGAAAAGGAGATATAGCACACAAGTAGACCT
GATCTAGCAGACCAACTAATTATCTGTATTATTGATTGTTTTTCAGAAATCTGCTATA
AGAAAAGCCATATTAGGACACAGAGTTAGTCTTAGGTTGTAATATCGAGCAGGCATAGC
AAGGTAGGATCACTACAGTACTTGGCAATAGCAGCATTATTAACACCAAAAAGATAAAG
CCACCTTTGGCGAGTGTGAGGAACTGACAGAGGATAGATGGAACAAGCCCCAGAAGACC
AAGGGCCACAGAGGGAGCCATACAATGAATGGACACTAG

N17 (SEQ ID NO:29)

ATGGAAACAGATGGCAGGTGATGATTGTGTGGCAGGTAGACAGGATGAGGATTAGAACA
TGGAACAGTTTAGTAAAAATACCATATGTATAGATCAAAGAAAGCTAGGGAAATGGTTTTAT
AGACATCACTATCAAAGTCCTCATCCAAAAGTAAGTTCAGAAGTACACATCCCCTAGAG
GATGCTAGATTGGAATAACACATATTGGGGTCTGCATACAGGAGAAAGAGACTGGCAT
TTGGGTCAGGGAGTCTCCATAGAATGGAGGAAAAGGAGATATAGCACACAAGTAGACCT
GATCTAGCAGACCAACTAATTATCTGTATTATTGATTGTTTTTCAGAAATCTGCTATA
AGAAAAGCCATATTAGGACACAGAGTTAGTCTTAGGTTGTAATATCGAGCAGGCATAGC
AAGGTAGGATCACTACAGTACTTGGCAATAGCAGCATTATTAACACCAAAAAGATAAAG
CCACCTTTGGCGAGTGTGAGGAACTGACAGAGGATAGATGGAACAAGCCCCAGAAGACC
AAGGGCCACAGAGGGAGCCATACAATGAATGGACACTAG

N22 (SEQ ID NO:30)

ATGGAAACAGATGGCAGGTGATGATTGTGTGGCAGGTAGACAGGATGAGGATTAGAACA
TGGAACAGTTTAGTAAACATACCATATGTATAGATCACAGAAAGCTAGGGAAATGGTTTTAT
AGACATCACTATCACAGTCTCATCCAAAAGTAAGTTCAGAAGTCCACATCCCCTAGAG
GATGCTAGATTGGCAATACCAACATTTTGGGGTCTGCATACAGGAGAAAGAGACTGGCAT
TTGGGTCAGGGAGTCTCCATAGAATGGAGGAAAAGGAGATATAGCACACAAGTAGACCT
GATCTAGCAGACCAACTAATTATCTGTATTATTGATTGTTTTTCAGAAATCTGCTATA
AGAAAAGCCATATTAGGACACAGAGTTAGTCTTAGGTTGTAATATCGAGCAGGCATAGC
AAGGTAGGATCACTACAGTACTTGGCAATAGCAGCATTATTAACACCAAAAAGATAAAG
CCACCTTTGGCGAGTGTGAGGAACTGACAGAGGATAGATGGAACAAGCCCCAGAAGACC
AAGGGCCACAGAGGGAGCCATACAATGAATGGACACTAG

FIGURE 8B

N23 (SEQ ID NO:31)

ATGGA AAAACAGATGGCAGGTGATGATTGTGTGGCAGGTAGACAGGATGAGGATTAGAACA
TGGAACAGTTTGTAGTAAAATACCATATGTATAGATCAAAGAAAGCTAGGGAATGGTTTTAT
AGACATCACTATCAAAGTCCTCATCCAAAAGTAAAGTTCAGAAGTCCACATCCCCTAGAG
GATGCTAGATTGGTAATTAACAACATATTGGGGTCTGCATACAGGAGAAAGAGACTGGCAT
TTGGGT CAGGGAGTCTCCATAGAATGGAGGAAAAGGAGATATAGCACACACGTCGACCCCT
GATCTCGACAGCCACTAATTTCATCTGTGTTATTTTGGATTGCTTTT CAGAATCTGCTATA
AGAAAAGCCATATTAGGACACAGAGTTAGTCCTAGGTGTGAATATCGAGCAGGACATAGC
AAGGTAGGATCACTACAGTACTTGGCAATAGCAGCATTAAATAACACCAAAAAAGATAAAG
CCACCTTTGGCCGAGTGT CAGGAAACTGACAGAGGATAGATGGAACAAGCCCCAGAAGACC
AAGGGCCACAGAGGGAGCCATACAATGAATGGACACTAG

N24 (SEQ ID NO:32)

ATGGA AAAACAGATGGCAGGTGATGATTGTGTGGCAGGTAGACAGGATGAGGATTAGAACA
TGGAACAGTTTGTAGTAAAATACCATATGTATAGATCAAAGAAAGCTAGGGAATGGTTTTAT
AGACATCACTATCAAAGTCCTCATCCAAAAGTAAAGTTCAGAAGTACACATCCCCTAGAG
GATGCTAGATTGGTAATTAACAACATATTGGGGTCTGCATACAGGAGAAAGAGACTGGCAT
TTGGGT CAGGGAGTCTCCATAGAATGGAGGAAAAGGAGATATAGCACACACGTAGACCCCT
GATCTAGCAGACCAACTAATTCATCTGTATTATTTTGGATTGTTTTT CAGAATCTGCTATA
AGAAAAGCCATATTAGGACACAGAGTTAGTCTAGGTGTGAATATCGAGCAGGACATAGC
AAGGTAGGATCACTACAGTACTTGGCAATAGCAGCATTAAATAACACCAAAAAAGATAAAG
CCACCTTTGGCCGAGTGT CAGGAAACTGACAGAGGATAGATGGAACAAGCCCCAGAAGACC
AAGGGCCACAGAGGGAGCCATACAATGAATGGACACTAG

N26 (SEQ ID NO:33)

ATGGA AAAACAGATGGCAGGTGATGATTGTGTGGCAGGTAGACAGGATGAGGATTAGAACA
TGGAACAGTTTGTAGTAAAATACCATATGTATAGATCAAAGAAAGCTAGGGAATGGTTTTAT
AGACATCACTATCAAAGTCCTCATCCAAAAGTAAAGTTCAGAAGTACACATCCCCTAGAG
GATGCTAGATTGGTAATTAACAACATATTGGGGTCTGCATACAGGAGAAAGAGACTGGCAT
TTGGGT CAGGGAGTCTCCATAGAATGGAGGAAAAGGAGATATAGCACACAAGTAGACCCCT
GATCTAGCAGACCACTAATTCATCTGTATTATTTTGGATTGTTTTT CAGAATCTGCTATA
AGAAAAGCCATATTAGGACACAGAGTTAGTCTAGGTGTGAATATCGAGCAGGACATAGC
AAGGTAGGATCACTACAGTACTTGGCAATAGCAGCATTAAATAACACCAAAAAAGATAAAG
CCACCTTTGGCCGAGTGT CAGGAAACTGACAGAGGATAGATGGAACAAGCCCCAGAAGACC
AAGGGCCACAGAGGGAGCCATACAATGAATGGACACTAG

N27 (SEQ ID NO:34)

ATGGA AAAACAGATGGCAGGTGATGATTGTGTGGCAGGTAGACAGGATGAGGATTAGAACA
TGGAACAGTTTGTAGTAAAATACCATATGTATAGATCAAAGAAAGCTAGGGAATGGTTTTAT
AGACATCACTATCAAAGTCCTCATCCAAAAGTAAAGTTCAGAAGTACACATCCCCTAGAG
GATGCTAGATTGGTAATTAACAACATTTTGGGGTCTGCATACAGGAGAAAGAGACTGGCAT
TTGGGT CAGGGAGTCTCCATAGAATGGAGGAAAAGGAGATATAGCACACAAGTAGACCCCT
GATCTAGCAGACCACTAATTCATCTGTATTATTTTGGATTGTTTTT CAGAATCTGCTATA
AGAAAAGCCATATTAGGACACAGAGTTAGTCTAGGTGTGAATATCGAGCAGGACATAGC
AAGGTAGGATCACTACAGTACTTGGCAATAGCAGCATTAAATAACACCAAAAAAGATAAAG
CCACCTTTGGCCGAGTGT CAGGAAACTGACAGAGGATAGATGGAACAAGCCCCAGAAGACC
AAGGGT CACAGAGGGAGCCATACAATGAATGGACACTAG

FIGURE 8C

N29 (SEQ ID NO:35)

ATGGA AACAGATGGCAGGTGATGATTGTGTGGCAGGTAGACAGGATGAGGATTAGAACA
TGGAACAGTTT TAGTAAAAATACCATATGTATAGATCAAAGAAAGCTAGGGAATGGTTTAAT
AGACATCACTATCACCGTCTCATCCAAAGTAAGTTTCAGAAGTCCACATCCCACCTAGAG
GATGCTAGATTGGAATAACAACATTTTGGGGTCTGCATACAGGAGAAAGAGACTGGCAT
TTGGGT CAGGGAGTCTCCATAGAATGGAGGAAAAGGAGATATAGCACACAAGTAGACCT
GATCTAGCAGACCAACTAATTCATCTGTATTATTTTGATTGTTTTTCAGAATCTGCTATA
AGAAAAGCCATATTAGGACACAGAGTTAGTCTTAGTGTGTAATATCGAGCAGGACATAGC
AAGGTAGGATCACTACAGTACTTGGCAATAGCAGCATTAATAACACCAAAAAGATAAAG
CCACCTTTGCGGAGTGT CAGGAACTGACAGAGGATAGATGGAACAAGCCCCAGAAGAC
AAGGGCCACAGAGGGAGCCATACAATGAATGGACACTAG

N30 (SEQ ID NO:36)

ATGGA AACAGATGGCAGGTGATGATTGTGTGGCAGGTAGACAGGATGAGGATTAGAACA
TGGAACAGTTT TAGTAAAAATACCATATGTATTGTATCAAAGAAAAGAAAAGGGAATGGT
TTTATAGACATCACTATCACAGCCCTCATCCAGAACAAAGTTCAACAGCCACATCCC GC
TAGTGGATTGGTAGATTGGA AAAAATAGCAGTTTGGAGTCTGGATACAGGAGATGGCGTCT
GGCACAGGGGCGCATCGAGTCTCCATAGAATGGAGGAAAAGGAGATATAGCACACAAGTAG
ACCTGTATCTAGTAGACCAACTAATTCATCTGTATTATTTTGATTGTTTTTCAGAATCTG
CTATAAGAAAAGCCATATTAGGACACAGAGTTAGTCTTAGTGTGTAATATCGAGCAGGAC
ATAGCAAGGTAGGATCACTACAGTACTTGGCAATAGCAGCATTAATAACACCAAAAAGATA
TAAAGCCACCTTTGCGGAGTGT CAGGAACTGACAGAGGATAGATGGAACAAGCCCCAGA
AGACCAAGGGCCACAGAGGGAGCCATACAATGAATGGACACTAG

T3 (SEQ ID NO:37)

ATGGA AACAGATGGCAGGTGATGATTGTGTGGCAAGTAGACAGGATGAGGATTAGAACA
TGGAACAGTTT TAGTAAAAACCATATGTATGTTTCAAAGAAAGCTAAGAAATGGTTTTAT
AGACATCACTATGAAAGCCCTCATCCAAAGTAAGTTCAACAGCCCATCCGCTAGGG
GATGGTAGATTGGAGAAAACAGCAGTTTGGAGTCTGCAGGCAGGAGATGGAGTCTGGCAC
AGGGGGCATCCAGTCTCCATAGAATGGAGGAAAAGGAGATATAGCACACAAGTAGACCT
GATTTGGTAGACCAACTAATTCATCTGTATTATTTTGATTGTTTTTCAGAATCTGCTATA
AGAAAGCCATATTAGGATATAGAGTTAGTCTTAGTGTGTAATACCAAGCAGGACATAAT
AAGGTAGGATCTCTACAGTACTTGGCACTAGCAGCATTAATAACACCAAAAAGATAAAG
CCACCTTTGCGCTAGTGTTAGGAACTGACAGAGGATAGATGGAACAAGCCCCAGAAGAC
AAGGGCCACAGAGGGAGCCATACAATGAATGGACACTAG

T4 (SEQ ID NO:38)

ATGGA AACAGATGGCAGGTGATGATTGTGTGGCAAGTAGACAGGATGAGGATTAGAGCA
TGGAACAGTTT TAGTAAAAACCATATGTATGTTTCAAAGAAAGCTAGGACATGGTTTTCT
AGACATCACTATGGAAGCCCTCATCCAAAGTATGTTTCAGAAGTACATCCCACTAGGG
GCTGCTAGATTGGTGATAACAACATATTGGAGTCTGCATGCAGGAGAAATGAGACTGGCAT
GTGGGTCAGAGAGTCTCCATAGAATGGAGGAAAAGGAGATATAGCACACAAGTAGACCT
GACTTGGCAGACCAACTAATTCATCTGTATTATTTTGATTGTTTTTCAGAATCTGCTATA
AGAAAAGCCATATTAGGATATAGAGTTAGTCTTAGTGTGTAATACCAAGCAGGACATAAT
AAGGTAGGATCTCTACAGTACTTGGCACTAGCAGCATTAATAACACCAAAAAGATAAAG
CCACCTTTGCGCTAGTGTGAGGAACTGACAGAGGATAGATGGAACAAGCCCCAGAAGACC
AAGGGCCACAGAGGGAGCCATACAATGAATGGACACTAG

FIGURE 8D

T35 (SEQ ID NO:39)

ATGGAACACAGATGGCAGGTGATGATTGTGTGGCAAGTAGACAGGATGAGGATTAGAGCA
 TGGAACAGTTTAGTAAAAACCCATATGTTATTTTCAAAGAAAGCTAAGAAATGGTTTTAT
 AGACATCACTATGAAAGCCCTCATCCAAACGTAAGTTCAGAAGTACACATCCCAGTAGGG
 GATGCTAGATTGGTGACAACACCATATTGGGGTCTGCATGGAGGAGAAAGAGACTGGTAT
 CTGGCTCAGGGAGTCTCCATAGAATGGAGGAAAAGGAGATATAGCACACAAGTAGACCCCT
 GACCTGGCAGACCAACTAATTCATCTGTATTATTTTGATTGTTTTTCAGAATCTGCTATA
 AGAAAAGCCATATTAGGATATAGAGTTAGTCTTAGGTGTGAATACCAAGCAGGACATAAT
 AAGGTAGGATCTCTACAGTACTTGGCACTAGCAGCATTAATAACACCAAAGAAGATAAAG
 CCACCTTTGCCTAGTGTGAGGAAACTGACAGAGGATAGATGGAACAAGCCCCAGAAGACC
 AAGGGCCACAGAGGGAGCCATACAATGAATGGACACTAG

T37 (SEQ ID NO:40)

ATGGAACACAGATGGGAGGTGATGATTGTGTGGGAAGTAGACAGGATGAGGATTAGAGCA
 TGGAACAGTTTAGTAAAAACCCATATGTTATTTCAAAGAAAGCTAAGAAATGGTTTTAT
 AGACATCACTATGAAAGCCCTCATCCAAAGTAAGTTCAGAAGTACACATCCCAGTAGGG
 GATGCTAGATTGGTGATAACAACATATTGGGGTCTGCATGCAGGAGAAAGAGACTGGCAT
 TTGGGTGAGGGAGTCTCCATAGAATGGAGGAAAAGGAGATATAGCACACAAGTAGACCCCT
 GACCTGGCAGACCAACTAATTCATCTGTATTATTTTGATTGTTTTTCAGAATCTGCTATA
 AGAAAAGCCATATTAGGATATAGAGTTAGTCTTAGGTGTGAATACCAAGCAGGACATAAT
 AAGGTAGGATCTCTACAGTACTTGGCACTAGCAGCATTAATAACACCAAAGAAGATAAAG
 CCACCTTTGCCTAGTGTGAGGAAACTGACAGAGGATAGATGGAACAAGCCCCAGAAGACC
 AAGGGCCACAGAGGGAGCCATACAATGAATGGACACTAG

T38 (SEQ ID NO:41)

ATGGAACACAGATGGCAGGTGATGATTGTGTGGCAAGTAGACAGGATGAGGATTAGAGCA
 TGGAACAGTTTAGTAAAAACCCATATGTTATTTCAAAGAAAGCTAAGAAATGGTTTTAT
 CGACATCACTATGACAGCCCTCATCCAGTCCAAAGTTCAACAGCCCATCCCGTAGGG
 GATGCTAGATTGCAGAAAATAGCATTTTGGAGTCTGGATGCAGGAGAAAGAGACTGGCAT
 TTGGGTGAGGGAGTCTCCATAGAATGGAGGAAAAGGAGATATAGCACACAAGTAGACCCCT
 GACCTGGCAGACCAACTAATTCATCTGTATTATTTTGATTGTTTTTCAGAATCTGCTATA
 AGAAAAGCCATATTAGGATATAGAGTTAGTCTTAGGTGTGAATACCAAGCAGGACATAAT
 AAGGTAGGATCTCTACAGTACTTGGCACTAGCAGCATTAATAACACCAAAGAAGATAAAG
 CCACCTTTGCCTAGTGTGAGGAAACTGACAGAGGATAGATGGAACAAGCCCCAGAAGACC
 AAGGGCCACAGAGGGAGCCATACAATGAATGGACACTAG

T39 (SEQ ID NO:42)

ATGGAACACAGATGGCAGGTGATGATTGTGTGGCAAGTAGACAGGATGAGGATTAGAGCA
 TGGAACAGTTTAGTAAAAACCCATATGTTATTTCAAAGAAAGCTAAGAAATGGTTTTAT
 AGACATCACTATGACAGCCCTCATCCAAAGTAAGTTCAGAAGTACACATCCCAGTAGGG
 GATGCTAGATTGGAGATAACAACATATTGGGGTCTGCATGCAGGAGAAAGAGACTGGCAT
 TTGGGTGAGGGAGTCTCCATAGAATGGAGGAAAAGGAGATATAGCACACAAGTAGACCCCT
 GACCTGGCAGACCAACTAATTCATCTGTATTATTTTGATTGTTTTTCAGAATCTGCTATA
 AGAAAAGCCATATTAGGATATAGAGTTAGTCTTAGGTGTGAATACCAAGCAGGACATAAT
 AAGGTAGGATCTCTACAGTACTTGGCACTAGCAGCATTAATAACACCAAAGAAGATAAAG
 CCACCTTTGCCTAGTGTGAGGAAACTGACAGAGGATAGATGGAACAAGCCCCAGAAGACC
 AAGGGCCACAGAGGGAGCCATACAATGAATGGACACTAG

FIGURE 8E

T40 (SEQ ID NO:43)

ATGGAACACAGATGGCAGGTGATGATTGTGTGGCAAGTAGACAGGATGAGGATTAGAGCA
 TGGAACAGTTTAGTAAAAACCCATATGTATGTTTCAAAGAAAGCTAAGAAATGGTTTAT
 AGACATCACTATGAAAGCCCTCATCCAAAAGTAAGTTCAGAAGTACACATCCCACTAGGG
 GATGCTAGATTGGGATACAACATATTTGGGGTCTGCATGCAGGAGAAAGAGACTGGCAT
 TTGGGTGAGGGAGTCTCCATAGAATGGAGGAAAAGGAGATATAGCACACAAGTAGACCCCT
 GACTTGGCAGACCACTAACTCATCTGTATTATTTTGATTGTTTTTTCAGAATCTGCTATA
 AGAAAAGCCATATTAGGATATAGAGTTAGTCTAGGTGTAATACCAAGCAGGACATAAT
 AAGGTAGGATCTCTACAGTACTTGGCACTAGCAGCATTAAATAACCAAGAAAGATAAAG
 CCACCTTTGCCTAGTGTGAGGAAACTGACAGAGGATAGATGGAACAAGCCCCAGAAGACC
 AAGGGCCACAGAGGGAGCCATACAATGAATGGACACTAG

T42 (SEQ ID NO:44)

ATGGAACACAGATGGCAGGTGATGATTGTGTGGCAAGTAGACAGGATGAGGATTAGAGCA
 TGGAACAGTTTAGTAAAAACCCATATGTATGTTTCAAAGAAAGCTAAGAAATGGTTTAT
 AGACATCACTATGAAAGCCCTCATCCAAAAGTAAGTTCAGAAGTACACATCCCACTAGGG
 GATGCTAGATTGGAGATAACAACATTTTGGGGTCTGCATGCAGGAGAAAGAGACTGGCAT
 TTGGGTGAGGGAGTCTCCATAGAATGGAGGAAAAGGAGATATAGCACACAAGTAGACCCCT
 GACTTGGCAGACCACTAACTCATCTGTATTATTTTGATTGTTTTTTCAGAATCTGCTATA
 AGAAAAGCCATATTAGGATATAGAGTTAGTCTAGGTGTAATACCAAGCAGGACATAAT
 AAGGTAGGATCTCTACAGTACTTGGCACTAGCAGCATTAAATAACCAAGAAAGATAAAG
 CCACCTTTGCCTAGTGTGAGGAAACTGACAGAGGATAGATGGAACAAGCCCCAGAAGACC
 AAGGGCCACAGAGGGAGCCATACAATGAATGGACACTAG

T43 (SEQ ID NO:45)

ATGGAACACAGATGGCAGGTGATGATTGTGTGGCAAGTAGACAGGATGAGGATTAGAGCA
 TGGAACAGTTTAGTAAAAACCCATATGTATGTTTCAAAGAAAGCTAAGAAATGGTTTAT
 AGACATCACTATGAAAGCCCTCATCCAAAAGTAAGTTCAGAAGTACACATCCCACTAGGG
 GATGCTAGATTGGAGATAACAACATTTTGGGGTCTGCATGCAGGAGAAAGAGACTGGCAT
 TTGGGTGAGGGAGTCTCCATAGAATGGAGGAAAAGGAGATATAGCACACAAGTAGACCCCT
 GACTTGGCAGACCACTAATTCATCTGTATTATTTTGGTTGTTTTTTCAGAATCTGCTATA
 AGAAAAGCCATATTAGGATATAGAGTTAGTCTAGGTGTAATACCAAGCAGGACATAAT
 AAGGTAGGATCTCTACAGTACTTGGCACTAGCAGCATTAAATAACCAAGAAAGATAAAG
 CCACCTTTGCCTAGTGTGAGGAAACTGACAGAGGATAGATGGAACAAGCCCCAGAAGACC
 AAGGGCCACAGAGGGAGCCATACAATGAATGGACACTAG

T44 (SEQ ID NO:46)

ATGGAACACAGATGGCAGGTGATGATTGTGTGGCAAGTAGACAGGATGAGGATTAGAGCA
 TGGAACAGTTTAGTAAAAACCCATATGTATGTTTCAAAGAAAGCTAAGAAATGGTTTAT
 AGACATCACTATGAAAGCCCTCATCCAAAAGTAAGTTCAGAAGTACACATCCCACTAGGG
 GATGCTAGATTGGAGATAACAACATATTTGGGGTCTGCATGCAGGAGAAAGAGACTGGCAT
 TTGGGTGAGGGAGTCTCCATAGAATGGAGGAAAAGGAGATATAGCACACAAGTAGACCCCT
 GACTTGGCAGACCACTAATTCATCTGTATTATTTTGGTTGTTTTTTCAGAATCTGCTATA
 AGAAAAGCCATATTAGGATATAGAGTTAGTCTAGGTGTAATACCAAGCAGGACATAAT
 AAGGTAGGATCTCTACAGTACTTGGCACTAGCAGCATTAAATAACCAAGAAAGATAAAG
 CCACCTTTGCCTAGTGTGAGGAAACTGACAGAGGATAGATGGAACAAGCCCCAGAAGACC
 AAGGGCCACAGAGGGAGCCATACAATGAATGGACACTAG

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In Re Application of: Velpandi AYYAVOO;
Thanadavarayan NAGASHUNMUGAM and David
B. WEINER

International Patent Application No.
PCT/US98/19478

International Filing Date: 18 September 1998

U.S. Serial No. 09/486625
Filing Date: 18 September 1998

For:
ATTENUATED VIF DNA IMMUNIZATION
CASSETTES FOR GENETIC VACCINES

DECLARATION AND POWER OF ATTORNEY

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name; and

I believe that I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a

☒ Utility Patent ☐ Design Patent

is sought on the invention, whose title appears above, the specification of which:

☒ was filed on September 18, 1998 in the PCT/US/RO under
International Serial No. PCT/US98/19478 .

☐ said application having been amended on _____ .

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose to the U.S. Patent and Trademark Office all information known to be material to the patentability of this application in accordance with 37 CFR § 1.56.

I hereby claim foreign priority benefits under 35 U.S.C. § 119(a-d) of any **foreign application(s)** for patent or inventor's certificate listed below and have also identified below any foreign application for patent or inventor's certificate having a filing date before that of any application on which priority is claimed:

Priority Claimed (If X'd)	Country	Serial Number	Date Filed
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I hereby claim the benefit under 35 U.S.C. § 120 of any United States application(s) listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States application in the manner provided by the first paragraph of 35 U.S.C. § 112, I acknowledge the duty to disclose to the U.S. Patent and Trademark Office all information known to be material to patentability as defined in 37 CFR § 1.56 which became available between the filing date of the prior application and the national or PCT international filing date of this application:

Serial Number	Date Filed	Patented/Pending/Abandoned
---------------	------------	----------------------------

I hereby claim the benefit under 35 U.S.C. § 119(e) of any United States provisional application(s) listed below:

Serial Number	Date Filed
60/059,283	September 18, 1997
60/060,172	September 26, 1997

I hereby appoint the following persons of the firm of **WOODCOCK WASHBURN KURTZ MACKIEWICZ & NORRIS LLP**, One Liberty Place - 46th Floor, Philadelphia, Pennsylvania 19103 as attorney(s) and/or agent(s) to prosecute this application and to transact all business in the Patent and Trademark Office connected therewith:

<u>Mark DeLuca</u>	Reg. No. <u>33,229</u>
<u>Paul K. Legaard</u>	Reg. No. <u>38,534</u>

TRANSMITTAL LETTER TO THE UNITED STATES
DESIGNATED/ELECTED OFFICE (DO/EO/US)
CONCERNING A FILING UNDER 35 U.S.C. 371

U.S. APPLICATION NO. (if known see 37 C.F.R. 1.5)

09/486625

INTERNATIONAL APPLICATION NO.
PCT/US98/19478INTERNATIONAL FILING DATE
18 September 1998PRIORITY DATE CLAIMED (earliest)
18 September 1997TITLE OF INVENTION
ATTENUATED VIF DNA IMMUNIZATION CASSETTES FOR GENETIC VACCINESAPPLICANT(S) FOR DO/EO/US
Velpandi AYYAVOO; Thanadavarayan NAGASHUNMUGAM and David B. WEINER

Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:

1. ☒ This is a **FIRST** submission of items concerning a filing under 35 U.S.C. 371.
2. ☐ This is a **SECOND** or **SUBSEQUENT** submission of items concerning a filing under 35 U.S.C. 371.
3. ☒ This express request to begin national examination procedures (35 U.S.C. 371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. 371(b) and PCT Articles 22 and 39(1).
4. ☒ A proper Demand for International Preliminary Examination was made by the 19th month from the earliest claimed priority date.
5. ☒ A copy of the International Application as filed (35 U.S.C. 371(c)(2)).
 - a. ☐ is transmitted herewith (required only if not transmitted by the International Bureau).
 - b. ☐ has been transmitted by the International Bureau.
 - c. ☒ is not required, as the application was filed in the United States Receiving Office (RO/US)
 - d. ☐ A translation of the International Application into English (35 U.S.C. 371(c)(2)).
6. ☒ Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. 371(c)(3))
 - a. ☐ are transmitted herewith (required only if not transmitted by the International Bureau).
 - b. ☐ have been transmitted by the International Bureau.
 - c. ☐ have not been made; however, the time limit for making such amendments has NOT expired.
 - d. ☒ have not been made and will not be made.
7. ☐ A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. 371(c)(3)).
8. ☐ An oath or declaration of the inventor(s) 35 U.S.C. 371(c)(4).
9. ☐ A translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371(c)(5)).
10. ☐ Items 11. to 16. below concern other document(s) or information included:
 11. ☐ An Information Disclosure Statement under 37 CFR 1.97 and 1.98.
 12. ☐ An assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included.
 13. ☐ A FIRST preliminary amendment.
 14. ☐ A SECOND or SUBSEQUENT preliminary amendment.
 15. ☐ A substitute specification.
 16. ☐ A change of power of attorney and/or address letter.
 17. ☒ Other items or information:
 - A copy of the Published PCT application, including the Search Report.
 - A copy of the International Preliminary Examination Report.
 - A sequence listing in computer readable form.

EXPRESS MAIL Mailing Label No. EL531430471US

Date of Deposit: February 29, 2000

I hereby certify that this paper or fee is being deposited with the United States Postal Service "Express Mail Post Office to Addressee" service under 37 CFR 1.10 on the date indicated above and is addressed to the Assistant Commissioner for Patents, Washington, D.C. 20231

MAILER Shelby McKnightSIGNATURE Shelby McKnight

U.S. APPLICATION NO. (37 CFR 1.53)

097486625

INTERNATIONAL APPLICATION NO.
PCT/US98/19478ATTORNEY DOCKET NUMBER
UPAP-028717. ☒ The following fees are submitted:**Basic National Fee (37 CFR 1.492(a)(1)-(5)):**

Search Report has been prepared by the EPO or JPO.....\$930.00

International preliminary examination fee paid to USPTO (37 CFR 1.482)

.....\$720.00

No international preliminary examination fee paid to USPTO (37 CFR 1.482) but

international search fee paid to USPTO (37 CFR 1.445(a)(2)).....\$790.00

Neither international preliminary examination fee (37 CFR 1.482) nor international
search fee (37 CFR 1.445(a)(2)) paid to USPTO.....\$1,070.00International preliminary examination fee paid to USPTO (37 CFR 1.482) and all
claims satisfied provisions of PCT Article 33(2)-(4).....\$98.00**ENTER APPROPRIATE BASIC FEE AMOUNT =**CALCULATIONS PTO USE ONLY

\$ 98.00

Surcharge of \$130.00 for furnishing the oath or declaration later than _ 20 _ 30 months from
the earliest claimed priority date (37 CFR 1.492(e)).

\$

Claims

Number Filed

Number Extra

Rate

Total claims

20 - 20 =

0

X \$22.00

\$

Independent Claims

5 - 3 =

2

x \$82.00

\$164.00

Multiple dependent claims(s) (if applicable)

+ \$270.00

\$

TOTAL OF ABOVE CALCULATIONS =

\$262.00

Reduction by 1/2 for filing by small entity, if applicable. Verified Small Entity statement must
also be filed. (Note 37 CFR 1.9, 1.27, 1.28).

\$

SUBTOTAL =

\$262.00

Processing fee of \$130.00 for furnishing the English translation later than the _ 20 _ 30 months
from the earliest claimed priority date (37 CFR 1.492(f)).

+

\$

TOTAL NATIONAL FEE =

\$262.00

Fee for recording the enclosed assignment (37 CFR 1.21(h)). The assignment must be
accompanied by an appropriate cover sheet (37 CFR 3.28, 3.31). \$40.00 per property

+

TOTAL FEES ENCLOSED =

\$262.00

Amount to be
refunded

\$

charged

\$

a. ☒ A check in the amount of \$ 262.00 to cover the above fee is enclosed.b. ☐ Please charge my Deposit Account No. 23-3050 in the amount of \$ _____ to cover the above fees. A duplicate copy of this sheet is
enclosed.c. ☒ The Commissioner if hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit
Account No. 23-3050. A duplicate copy of this sheet is enclosed.**NOTE:** Where an appropriate time limit under 37 CFR 1.494 or 1.495 has not been met, a petition to revive (37 CFR 1.137(a) or (b))
must be filed and granted to restore the application to pending status.**SEND ALL CORRESPONDENCE TO:**Paul K. Legaard
Woodcock Washburn Kurtz
Mackiewicz & Norris LLP
One Liberty Place - 46th Floor
Philadelphia, PA 19103
(215) 568-3100

SIGNATURE

Paul K. Legaard

NAME

38,534

REGISTRATION NUMBER


Address all telephone calls and correspondence to:

Mark DeLuca / Paul K. Legaard
WOODCOCK WASHBURN KURTZ
MACKIEWICZ & NORRIS LLP
One Liberty Place - 46th Floor
Philadelphia PA 19103
 Telephone No.: (215) 568-3100
 Facsimile No.: (215) 568-3439

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

10 Name: <u>Velpandi AYYAVOO</u>	<u>Velpandi Ayyavoo</u> Signature
Mailing Address: 3410 Stonecliffe Drive Monroeville, PA 15146 <u>PA</u> USA	Date of Signature: <u>9/6/06</u>
City/State of Actual Residence: Monroeville, Pennsylvania	Citizenship: <u>India</u>

290 Name: <u>Thanadavarayan</u> <u>NAGASHUNMUGAM</u>	<u>Thanadavarayan</u> Signature
Mailing Address: 3410 Stonecliffe Drive Monroeville, PA 15146 <u>PA</u> USA	Date of Signature: <u>Sep 06 2006</u>
City/State of Actual Residence: Havertown, Pennsylvania	Citizenship: <u>India</u>

308 Name: <u>David B. WEINER</u>	
Mailing Address: 717 Beacom Lane <u>Merion Station, PA</u> 19066 <i>PA</i> USA	Signature Date of Signature: <u>9/11/00</u>
City/State of Actual Residence: Merion Station, Pennsylvania	Citizenship: <u>United States</u>

SEQUENCE LISTING

<110> Ayyavoo, Velpandi
 Nagashunmugam, Thandavarayan
 Weiner, David B.
 University of Pennsylvania

<120> ATTENUATED VIF DNA IMMUNIZATION CASSETTES FOR GENETIC
 VACCINES

<130> UPAP-0263

<140> HEREWITH

<141> 1998-09-18

<160> 46

<170> PatentIn Ver. 2.0

<210> 1

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 1 5 10 15

Arg Ile Arg Thr Trp Asn Ser Leu Val Lys His His Met Tyr Val Ser
 20 25 30

Lys Lys Ala Arg Trp Phe Tyr Arg His His Tyr Glu Ser Pro His Pro
 35 40 45

Lys Val Ser Ser Glu Val His Ile Pro Leu Gly Asp Ala Arg Leu Glu
 50 55 60

Thr Thr Thr Tyr Trp Gly Leu His Gly Glu Arg Asp Trp His Leu Gly
 65 70 75 80

Gln Gly Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr Gln Val
85 90 95

Asp Pro Asp Leu Ala Asp Gln Leu Ile His Leu Tyr Tyr Phe Asp Cys
100 105 110

Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly Tyr Arg Val Ser
115 120 125

Pro Arg Cys Glu Tyr Gln Ala Gly His Asn Lys Val Gly Ser Leu Gln
130 135 140

Tyr Leu Ala Leu Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys Pro Pro
145 150 155 160

Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys Pro Gln
165 170 175

Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His
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<210> 2

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<212> DNA

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<211> 190

<212> PRT

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<223> Description of Artificial Sequence: Novel Sequence

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Met Glu Asn Arg Trp Gln Val Ile Ile Val Trp Gln Val Asp Arg Met
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Arg Ile Arg Thr Trp Asn Ser Leu Val Lys Tyr His Met Tyr Ser Lys
 20 25 30

Lys Ala Arg Glu Trp Phe Tyr His His Tyr Gln Ser Pro His Pro Lys
 35 40 45

Val Ser Ser Glu Val His Ile Pro Leu Glu Asp Ala Arg Leu Glu Ile
 50 55 60

Thr Ser Phe Trp Gly Leu His Thr Gly Glu Arg Asp Trp His Leu Gly
 65 70 75 80

Gln Gly Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr His Val
 85 90 95

Asp Pro Asp Leu Ala Asp Gln Leu Ile His Leu Tyr Tyr Phe Asp Cys
 100 105 110

Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly His Arg Val Ser
 115 120 125

Pro Arg Cys Glu Tyr Arg Ala Gly His Ser Lys Val Gly Ser Leu Gln
 130 135 140

Tyr Leu Ala Ile Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys Pro Pro
 145 150 155 160

Leu Ala Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys Pro Gln
 165 170 175

Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His
 180 185 190

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Arg Ile Arg Thr Trp Asn Ser Leu Val Lys Tyr His Met Tyr Arg Ser
 20 25 30

Lys Lys Ala Arg Glu Trp Phe Tyr Arg His His Tyr Gln Ser Pro His
 35 40 45

Pro Arg Val Ser Ser Glu Val His Ile Pro Leu Glu Asp Ala Arg Leu
 50 55 60

Glu Ile Thr Thr Tyr Trp Gly Leu His Thr Gly Glu Arg Asp Trp His
 65 70 75 80

Leu Gly Gln Gly Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr
 85 90 95

Gln Val Asp Pro Asp Leu Ala Asp Gln Leu Ile His Leu Tyr Tyr Phe
 100 105 110

Asp Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly His Arg
 115 120 125

Val Ser Pro Arg Cys Glu Tyr Arg Ala Gly His Ser Lys Val Gly Ser
 130 135 140

Leu Gln Tyr Leu Ala Ile Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys
 145 150 155 160

Pro Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys
 165 170 175

Pro Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His
 180 185 190

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<211> 192

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Met Glu Asn Arg Trp Gln Val Met Ile Val Trp Gln Val Asp Arg Met

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Arg Ile Arg Thr Trp Asn Ser Leu Val Lys Tyr His Met Tyr Arg Ser

20

25

30

Lys Lys Ala Arg Glu Trp Phe Tyr Arg His His Tyr Gln Ser Pro His

35

40

45

Pro Lys Val Ser Ser Glu Val His Ile Pro Leu Glu Asp Ala Arg Leu

50

55

60

Glu Thr Thr Thr Tyr Trp Gly Leu His Thr Gly Glu Arg Asp Trp His

65

70

75

80

Leu Gly Gln Gly Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr

85

90

95

Gln Val Asp Pro Asp Leu Ala Asp Gln Leu Ile His Leu Tyr Tyr Phe

100

105

110

Asp Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly His Arg

115

120

125

Val Ser Pro Arg Cys Glu Tyr Arg Ala Gly His Ser Lys Val Gly Ser

130

135

140

Leu Gln Tyr Leu Ala Ile Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys

145

150

155

160

Pro Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys

165

170

175

Pro Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His

180

185

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<210> 7

<211> 192

<212> PRT

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<223> Description of Artificial Sequence: Novel Sequence

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1

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10

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Arg Ile Arg Thr Trp Asn Ser Leu Val Thr Tyr His Met Tyr Arg Ser

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25

30

Gln Lys Ala Arg Glu Trp Phe Asn Arg His His Tyr His Ser Pro His

35

40

45

Pro Lys Val Ser Ser Glu Val His Ile Pro Leu Glu Asp Ala Arg Leu

50

55

60

Ala Ile Pro Thr Phe Trp Gly Leu His Thr Gly Glu Arg Asp Trp His

65

70

75

80

Leu Gly Gln Gly Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr

85

90

95

Gln Val Asp Pro Asp Leu Ala Asp Gln Leu Ile His Leu Tyr Tyr Phe

100

105

110

Asp Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly His Arg

115

120

125

Val Ser Pro Arg Cys Glu Tyr Arg Ala Gly His Ser Lys Val Gly Ser

130

135

140

Leu Gln Tyr Leu Ala Ile Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys

145

150

155

160

Pro Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys

165

170

175

Pro Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His

180

185

190

<210> 8

<211> 192

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Novel Sequence

<400> 8

Met Glu Asn Arg Trp Gln Val Met Ile Val Trp Gln Val Asp Arg Met

1 5 10 15

Arg Ile Arg Thr Trp Asn Ser Leu Val Lys Tyr His Met Tyr Arg Ser

20 25 30

Lys Lys Ala Arg Glu Trp Phe Tyr Arg His His Tyr Gln Ser Pro His

35 40 45

Pro Lys Val Ser Ser Glu Val His Ile Pro Leu Glu Asp Ala Arg Leu

50 55 60

Glu Ile Thr Thr Tyr Trp Gly Leu His Thr Gly Glu Arg Asp Trp His

65 70 75 80

Leu Gly Gln Gly Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr

85 90 95

His Val Asp Pro Asp Leu Ala Asp His Leu Ile His Leu Cys Tyr Phe

100 105 110

Asp Cys Leu Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly His Arg

115 120 125

Val Ser Pro Arg Cys Glu Tyr Arg Ala Gly His Ser Lys Val Gly Ser

130 135 140

Leu Gln Tyr Leu Ala Ile Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys

145 150 155 160

Pro Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys

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Pro Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His

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<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Novel Sequence

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Met Glu Asn Arg Trp Gln Val Met Ile Val Trp Gln Val Asp Arg Met
 1 5 10 15

Arg Ile Arg Thr Trp Asn Ser Leu Val Lys Tyr His Met Tyr Arg Ser
 20 25 30

Lys Lys Ala Arg Glu Trp Phe Tyr Arg His His Tyr Gln Ser Pro His
 35 40 45

Pro Lys Val Ser Ser Glu Val His Ile Pro Leu Glu Asp Ala Arg Leu
 50 55 60

Val Ile Thr Thr Tyr Trp Gly Leu His Thr Gly Glu Arg Asp Trp His
 65 70 75 80

Leu Gly Gln Gly Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr
 85 90 95

His Val Asp Pro Asp Leu Ala Asp Gln Leu Ile His Leu Tyr Tyr Phe
 100 105 110

Asp Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly His Arg
 115 120 125

Val Ser Pro Arg Cys Glu Tyr Arg Ala Gly His Ser Lys Val Gly Ser
 130 135 140

Leu Gln Tyr Leu Ala Ile Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys
 145 150 155 160

Pro Pro Leu Ala Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys
 165 170 175

Pro Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His
 180 185 190

<210> 10

<211> 192

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Novel Sequence

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Arg Ile Arg Thr Trp Asn Ser Leu Val Lys Tyr His Met Tyr Arg Ser

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25

30

Lys Lys Ala Arg Glu Trp Phe Tyr Arg His His Tyr Gln Ser Pro His

35

40

45

Pro Lys Val Ser Ser Glu Val His Ile Pro Leu Glu Asp Ala Arg Leu

50

55

60

Val Ile Thr Thr Tyr Trp Gly Leu His Thr Gly Glu Arg Asp Trp His

65

70

75

80

Leu Gly Gln Gly Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr

85

90

95

Gln Val Asp Pro Asp Leu Ala Asp His Leu Ile His Leu Tyr Tyr Phe

100

105

110

Asp Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly His Arg

115

120

125

Val Ser Pro Arg Cys Glu Tyr Arg Ala Gly His Ser Lys Val Gly Ser

130

135

140

Leu Gln Tyr Leu Ala Ile Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys

145

150

155

160

Pro Pro Leu Ala Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys

165

170

175

Pro Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His

180

185

190

<210> 11

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<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

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10

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Arg Ile Arg Thr Trp Asn Ser Leu Val Lys Tyr His Met Tyr Arg Ser

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25

30

Lys Lys Ala Arg Glu Trp Phe Tyr Arg His His Tyr Gln Ser Pro His

35

40

45

Pro Lys Val Ser Ser Glu Val His Ile Pro Leu Glu Asp Ala Arg Leu

50

55

60

Val Ile Thr Thr Phe Trp Gly Leu His Thr Gly Glu Arg Asp Trp His

65

70

75

80

Leu Gly Gln Gly Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr

85

90

95

His Val Asp Pro Asp Leu Ala Asp Gln Leu Ile His Leu Tyr Tyr Phe

100

105

110

Asp Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly His Arg

115

120

125

Val Ser Pro Arg Cys Glu Tyr Arg Ala Gly His Ser Lys Val Gly Ser

130

135

140

Leu Gln Tyr Leu Ala Ile Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys

145

150

155

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Pro Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys

165

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175

Pro Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His

180

185

190

<210> 12

<211> 192

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Novel Sequence

<400> 12

Met Glu Asn Arg Trp Gln Val Met Ile Val Trp Gln Val Asp Arg Met

1

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10

15

Arg Ile Arg Thr Trp Asn Ser Leu Val Lys Tyr His Met Tyr Arg Ser

20

25

30

Lys Lys Ala Arg Glu Trp Phe Asn Arg His His Tyr His Arg Pro His

35

40

45

Pro Lys Val Ser Ser Glu Val His Ile Pro Leu Glu Asp Ala Arg Leu

50

55

60

Glu Ile Thr Thr Phe Trp Gly Leu His Thr Gly Glu Arg Asp Trp His

65

70

75

80

Leu Gly Gln Gly Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr

85

90

95

Gln Val Asp Pro Asp Leu Ala Asp Gln Leu Ile His Leu Tyr Tyr Phe

100

105

110

Asp Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly His Arg

115

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Val Ser Pro Arg Cys Glu Tyr Arg Ala Gly His Ser Lys Val Gly Ser

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135

140

Leu Gln Tyr Leu Ala Ile Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys

145

150

155

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Pro Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys

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Pro Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His

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<210> 13

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<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Novel Sequence

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Met Glu Asn Arg Trp Gln Val Met Ile Val Trp Gln Val Asp Arg Met

1

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10

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Arg Ile Arg Thr Trp Asn Ser Leu Val Lys Tyr His Met Tyr Arg Ser

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25

30

Gln Lys Glu Arg Glu Trp Phe Asn Arg His His Tyr His Ser Pro His

35

40

45

Pro Glu Gln Ser Ser Thr Ala His Ile Pro Leu Val Asp Gly Arg Leu

50

55

60

Glu Lys Ile Ala Val Trp Ser Leu Asp Thr Gly Glu Gly Val Trp His

65

70

75

80

Arg Gly His Arg Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr

85

90

95

Gln Val Asp Pro Asp Leu Val Asp Gln Leu Ile His Leu Tyr Tyr Phe

100

105

110

Asp Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly His Arg

115

120

125

Val Ser Pro Arg Cys Glu Tyr Arg Ala Gly His Ser Lys Val Gly Ser

130

135

140

Leu Gln Tyr Leu Ala Ile Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys

145

150

155

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Pro Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys

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Pro Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His

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185

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<210> 14

<211> 192

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Novel Sequence

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10

15

Arg Ile Arg Thr Trp Asn Ser Leu Val Lys His His Met Tyr Val Ser

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30

Lys Lys Ala Lys Lys Trp Phe Tyr Arg His His Tyr Glu Ser Pro His

35

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Pro Lys Val Ser Ser Thr Ala His Ile Pro Leu Gly Asp Gly Arg Leu

50

55

60

Glu Lys Thr Ala Val Trp Ser Leu Gln Ala Gly Asp Gly Val Trp His

65

70

75

80

Arg Gly His Pro Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr

85

90

95

Gln Val Asp Pro Asp Leu Val Asp Gln Leu Ile His Leu Tyr Tyr Phe

100

105

110

Asp Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly Tyr Arg

115

120

125

Val Ser Pro Arg Cys Glu Tyr Gln Ala Gly His Asn Lys Val Gly Ser

130

135

140

Leu Gln Tyr Leu Ala Leu Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys

145

150

155

160

Pro Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys

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Pro Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His

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<210> 15

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Novel Sequence

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Met Glu Asn Arg Trp Gln Val Met Ile Val Trp Gln Val Asp Arg Met
 1 5 10 15

Arg Ile Arg Ala Trp Asn Ser Leu Val Lys His His Met Tyr Val Ser
 20 25 30

Lys Lys Ala Arg Thr Trp Phe Ser Arg His His Tyr Gly Ser Pro His
 35 40 45

Pro Lys Val Cys Ser Glu Val His Ile Pro Leu Gly Asp Ala Arg Leu
 50 55 60

Val Ile Thr Thr Tyr Trp Ser Leu His Ala Gly Glu Asp Trp His Val
 65 70 75 80

Gly Gln Arg Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr Gln
 85 90 95

Val Asp Pro Asp Leu Ala Asp Gln Leu Ile His Leu Tyr Tyr Phe Asp
 100 105 110

Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly Tyr Arg Val
 115 120 125

Ser Pro Arg Cys Glu Tyr Gln Ala Gly His Asn Lys Val Gly Ser Leu
 130 135 140

Gln Tyr Leu Ala Leu Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys Pro
 145 150 155 160

Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys Pro
 165 170 175

Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His
 180 185 190

<210> 16

<211> 192

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 16

Met Glu Asn Arg Trp Gln Val Met Ile Val Trp Gln Val Asp Arg Met

1

5

10

15

Arg Ile Arg Ala Trp Asn Ser Leu Val Lys His His Thr Tyr Phe Ser

20

25

30

Lys Lys Ala Lys Lys Trp Phe Tyr Arg His His Tyr Glu Ser Pro His

35

40

45

Pro Asn Val Ser Ser Glu Val His Ile Pro Leu Gly Asp Ala Arg Leu

50

55

60

Val Thr Thr Pro Tyr Trp Gly Leu His Gly Gly Glu Arg Asp Trp Tyr

65

70

75

80

Leu Ala Gln Gly Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr

85

90

95

Gln Val Asp Pro Asp Leu Ala Asp Gln Leu Ile His Leu Tyr Tyr Phe

100

105

110

Asp Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly Tyr Arg

115

120

125

Val Ser Pro Arg Cys Glu Tyr Gln Ala Gly His Asn Lys Val Gly Ser

130

135

140

Leu Gln Tyr Leu Ala Leu Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys

145

150

155

160

Pro Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys

165

170

175

Pro Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His

180

185

190

<210> 17

<211> 192

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 17

Met Glu Asn Arg Trp Glu Val Met Ile Val Trp Glu Val Asp Arg Met

1

5

10

15

Arg Ile Arg Ala Trp Asn Ser Leu Val Lys His His Met Tyr Val Ser

20

25

30

Lys Lys Ala Lys Lys Trp Phe Tyr Arg His His Tyr Glu Ser Pro His

35

40

45

Pro Lys Val Ser Ser Glu Val His Ile Pro Leu Gly Asp Ala Arg Leu

50

55

60

Val Ile Thr Thr Tyr Trp Gly Leu His Ala Gly Glu Arg Asp Trp His

65

70

75

80

Leu Gly Gln Gly Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr

85

90

95

Gln Val Asp Pro Asp Leu Ala Asp Gln Leu Ile His Leu Tyr Tyr Phe

100

105

110

Asp Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly Tyr Arg

115

120

125

Val Ser Pro Arg Cys Glu Tyr Gln Ala Gly His Asn Lys Val Gly Ser

130

135

140

Leu Gln Tyr Leu Ala Leu Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys

145

150

155

160

Pro Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys

165

170

175

Pro Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His

180

185

190

<210> 18

<211> 192

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 17

Met Glu Asn Arg Trp Gln Val Met Ile Val Trp Gln Val Asp Arg Met

1

5

10

15

Arg Ile Arg Ala Trp Asn Ser Leu Val Lys His His Met Tyr Val Ser

20

25

30

Lys Asn Ala Lys Lys Trp Phe Tyr Arg His His Tyr Asp Ser Pro His

35

40

45

Pro Val Gln Ser Ser Thr Ala His Ile Pro Leu Gly Asp Gly Arg Leu

50

55

60

Gln Lys Ile Ala Phe Trp Ser Leu Asp Ala Gly Glu Arg Asp Trp His

65

70

75

80

Leu Gly Gln Gly Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr

85

90

95

Gln Val Asp Pro Asp Leu Ala Asp Gln Leu Ile His Leu Tyr Tyr Phe

100

105

110

Asp Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly Tyr Arg

115

120

125

Val Ser Pro Arg Cys Glu Tyr Gln Ala Gly His Asn Lys Val Gly Ser

130

135

140

Leu Gln Tyr Leu Ala Leu Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys

145

150

155

160

Pro Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys

165

170

175

Pro Gln Lys Thr Lys Gly His Arg Gly Arg His Thr Met Asn Gly His

180

185

190

<210> 19

<211> 192

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 19

Met Glu Asn Arg Trp Gln Val Met Ile Val Trp Gln Val Asp Arg Met

1

5

10

15

Arg Ile Arg Ala Trp Asn Ser Leu Val Lys His His Met Tyr Val Ser

20

25

30

Lys Lys Ala Lys Lys Trp Phe Tyr Arg His His Tyr Asp Ser Pro His

35

40

45

Pro Lys Val Ser Ser Glu Val His Ile Pro Leu Gly Asp Ala Arg Leu

50

55

60

Glu Thr Thr Thr Tyr Trp Gly Leu His Ala Gly Glu Arg Asp Trp His

65

70

75

80

Leu Gly Gln Gly Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr

85

90

95

His Val Asp Pro Asp Leu Ala Asp Gln Leu Ile His Leu Tyr Tyr Phe

100

105

110

Asp Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly Tyr Arg

115

120

125

Val Ser Pro Arg Cys Glu Tyr Gln Ala Gly His Asn Lys Val Gly Ser

130

135

140

Leu Gln Tyr Leu Ala Leu Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys

145

150

155

160

Pro Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys

165

170

175

Pro Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His

180

185

190

<210> 20

<211> 192

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 20

Met Glu Asn Arg Trp Gln Val Met Ile Val Trp Gln Val Asp Arg Met

1

5

10

15

Thr Ile Arg Ala Trp Asn Ser Leu Val Lys His His Met Tyr Val Ser

20

25

30

Lys Lys Ala Lys Lys Trp Phe Tyr Arg His His Tyr Glu Ser Pro His

35

40

45

Pro Lys Val Ser Ser Glu Val His Ile Pro Leu Gly Asp Ala Arg Leu

50

55

60

Val Ile Thr Thr Tyr Trp Gly Leu His Ala Gly Glu Arg Asp Trp His

65

70

75

80

Leu Gly Gln Gly Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr

85

90

95

Gln Val Asp Pro Asp Leu Ala Asp Gln Leu Thr His Leu Tyr Tyr Phe

100

105

110

Asp Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly Tyr Arg

115

120

125

Val Ser Pro Arg Cys Glu Tyr Gln Ala Gly His Asn Lys Val Gly Ser

130

135

140

Leu Gln Tyr Leu Ala Leu Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys

145

150

155

160

Pro Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys

165

170

175

Pro Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His

180

185

190

<210> 21

<211> 188

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 21

Met Glu Asn Arg Trp Gln Val Met Ile Val Trp Gln Val Asp Arg Met
 1 5 10 15

Arg Ile Arg Ala Trp Asn Ser Leu Val Lys His His Met Tyr Val Ser
 20 25 30

Lys Lys Ala Lys Lys Trp Phe Asn Arg His His Tyr Asp Arg Pro His
 35 40 45

Pro Lys Val Ser Ser Glu Val His Ile Pro Leu Gly Asp Ala Arg Leu
 50 55 60

Glu Ile Thr Thr Phe Trp Gly Leu His Ala Gly Glu Arg Asp Trp His
 65 70 75 80

Leu Gly Gln Arg Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr
 85 90 95

Gln Val Asp Pro Asp Leu Ala Asp Gln Leu Thr His Leu Tyr Tyr Phe
 100 105 110

Asp Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly Tyr Arg
 115 120 125

Val Ser Pro Arg Cys Glu Tyr Gln Ala Gly His Asn Lys Val Gly Ser
 130 135 140

Leu Gln Tyr Leu Ala Leu Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys
 145 150 155 160

Pro Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys
 165 170 175

Pro Gln Lys Thr Lys Gly Thr Glu Gly Ala Ile Gln
 180 185

<210> 22

<211> 192

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 22

Met Glu Asn Arg Trp Gln Val Met Ile Val Trp Gln Val Asp Arg Met

1

5

10

15

Arg Ile Arg Ala Trp Asn Ser Leu Val Lys His His Met Phe Val Ser

20

25

30

Lys Lys Ala Lys Lys Trp Phe Tyr Arg His His Tyr Glu Ser Pro His

35

40

45

Pro Lys Val Ser Ser Glu Val His Ile Pro Leu Gly Asp Ala Arg Leu

50

55

60

Glu Ile Thr Thr Phe Trp Gly Leu His Ala Gly Glu Arg Asp Trp His

65

70

75

80

Leu Gly Gln Gly Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr

85

90

95

Gln Val Asp Pro Asp Leu Ala Asp Gln Leu Ile His Leu Tyr Tyr Phe

100

105

110

Gly Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly Tyr Arg

115

120

125

Val Ser Pro Arg Cys Glu Tyr Gln Ala Gly His Asn Lys Val Gly Ser

130

135

140

Leu Gln Tyr Leu Gly Leu Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys

145

150

155

160

Pro Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys

165

170

175

Pro Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His

180

185

190

<210> 23

<211> 192

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 23

Met Glu Asn Arg Trp Gln Val Met Ile Val Trp Gln Val Asp Arg Met

1

5

10

15

Arg Ile Arg Ala Trp Asn Ser Leu Val Lys His His Met Tyr Val Ser

20

25

30

Lys Lys Ala Lys Lys Trp Phe Tyr Arg His His Tyr Glu Ser Pro His

35

40

45

Pro Gln Val Ser Ser Glu Val His Ile Pro Leu Gly Asp Ala Arg Leu

50

55

60

Glu Ile Thr Thr Tyr Trp Gly Leu His Ala Gly Glu Arg Asp Trp His

65

70

75

80

Leu Gly Gln Gly Val Ser Ile Glu Trp Arg Lys Arg Arg Tyr Ser Thr

85

90

95

Gln Val Asp Pro Asp Leu Ala Asp Gln Leu Ile His Leu Tyr Tyr Phe

100

105

110

Asp Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Ile Leu Gly Tyr Arg

115

120

125

Val Ser Pro Arg Cys Glu Tyr Gln Ala Gly His Asn Lys Val Gly Ser

130

135

140

Leu Gln Tyr Leu Ala Leu Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys

145

150

155

160

Pro Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys

165

170

175

Pro Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His

180

185

190

<210> 24

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 24

Ile Glu Trp Arg Lys Lys Arg Tyr

1

5

<210> 25

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 25

Asp Arg Trp Asn Lys Pro Gln

1

5

<210> 26

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 26

Ser Leu Gln Tyr Leu Ala

1

5

<210> 27

<211> 579

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 27

atggaaaaca gatggcaggt gattattgtg tggcaggtag acaggatgag gattagaaca 60
 tggacagtt tagtaaaata ccatatgtat tgatcaaga aagctaggga atggtttat 120
 tgacatcact atcaaatgcc tcatccaaaa gtaagttcag aagtacacat cccactagag 180
 gatgctagat tggaaataac atcatttgg ggtctgcata caggagaaa agactggcat 240
 ttgggtcagg gagtctccat agaattggagg aaaaggagat atagcacaca cgtcgacct 300
 gatctagcag accaactaat tcatctgtat tattttgatt gttttcaga atctgctata 360
 agaaaagcca tattaggaca cagagttagt cctagggtg aatatcgagc aggacatagc 420
 aaggttagat cactacagta ctggcgaata gcagcattaa taacaccaa aaagataaag 480
 ccacctttgc cgagtgtcag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
 aagggccaca gaggagacca tacaatgaat ggacactag 579

<210> 28

<211> 579

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 28

atggaaaaca gatggcaggt gatgattgtg tggcaggtag acaggatgag gattagaaca 60
 tggacagtt tagtaaaata ccatatgtat agatcaaga aagctaggga atggtttat 120
 agacatcact atcaaatgcc tcatcaaga gtaagttcag aagtacacat cccactagag 180
 gatgctagat tggaaataac aacatattgg ggtctgcata caggagaaa agactggcat 240
 ttgggtcagg gagtctccat agaattggagg aaaaggagat atagcacaca agtagacct 300
 gatctagcag accaactaat tcatctgtat tattttgatt gttttcaga atctgctata 360
 agaaaagcca tattaggaca cagagttagt cctagggtg aatatcgagc aggacatagc 420
 aaggttagat cactacagta ctggcgaata gcagcattaa taacaccaa aaagataaag 480
 ccacctttgc cgagtgtcag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
 aagggccaca gaggagacca tacaatgaat ggacactag 579

<210> 29

<211> 579

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 29

atggaaaaca gatggcaggt gatgattgtg tggcaggtag acaggatgag gattagaaca 60
 tggacagtt tagtaaaata ccatatgtat agatcaaga aagctaggga atggtttat 120
 agacatcact atcaaatgcc tcatccaaaa gtaagttcag aagtacacat cccactagag 180
 gatgctagat tggaaataac aacatattgg ggtctgcata caggagaaa agactggcat 240
 ttgggtcagg gagtctccat agaattggagg aaaaggagat atagcacaca agtagacct 300

gatctagcag accaactaat tcactgtat tattttgatt gttttcaga atctgctata 360
 agaaaagcca tattaggaca cagagttagt cctagggtgtg aatatcgagc aggcacatagc 420
 aaggtaggat cactacagta ctggcaata gcagcattaa taacacccaaa aaagataaag 480
 ccacctttgc cgagtgtcag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
 aagggccaca gagggagcca tacaatgaat ggacactag 579

<210> 30

<211> 579

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 30

atggaaaaca gatggcaggt gatgattgtg tggcaggtag acaggatgag gattagaaca 60
 tggaaacagt tagtaacata ccataatgat agatcacaga aagctaggga atggtttat 120
 agacatcact atcacagtcc tcactcaaaa gtaagttcag aagtcacat cccactagag 180
 gatgctagat tggcaatacc aacattttgg ggtctgcata caggagaaag agactggcat 240
 ttgggtcagg gagtctccat agaattggagg aaaaggagat atagcacaca agtagacct 300
 gatctcgag accaactaat tcactgtat tattttgatt gttttcaga atctgctata 360
 agaaaagcca tattaggaca cagagttagt cctagggtgtg aatatcgagc aggcacatagc 420
 aaggtaggat cactacagta ctggcaata gcagcattaa taacacccaaa aaagataaag 480
 ccacctttgc cgagtgtcag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
 aagggccaca gagggagcca tacaatgaat ggacactag 579

<210> 31

<211> 579

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 31

atggaaaaca gatggcaggt gatgattgtg tggcaggtag acaggatgag gattagaaca 60
 tggaaacagt tagtaaaata ccataatgat agatcaaaaa aagctaggga atggtttat 120
 agacatcact atcaaaagtc tcactcaaaa gtaagttcag aagtcacat cccactagag 180
 gatgctagat tggaaataac aacatattgg ggtctgcata caggagaaag agactggcat 240
 ttgggtcagg gagtctccat agaattggagg aaaaggagat atagcacaca cgtcgacct 300
 gatctcgag accaccta attcactgtgt tattttgatt gttttcaga atctgctata 360
 agaaaagcca tattaggaca cagagttagt cctagggtgtg aatatcgagc aggcacatagc 420
 aaggtaggat cactacagta ctggcaata gcagcattaa taacacccaaa aaagataaag 480
 ccacctttgc cgagtgtcag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
 aagggccaca gagggagcca tacaatgaat ggacactag 579

<210> 32
 <211> 579
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 32

atggaaaaca gatggcaggt gatgattgtg tggcaggtag acaggatgag gattagaaca 60
 tggaaacagtt tagtaaaata ccatatgtat agatcaaaga aagctaggga atggtttat 120
 agacatcact atcaaaagtc tcatccaaaa gtaagttcag aagtacacat cccactagag 180
 gatgctgatg ttgtaataac aacatattgg ggtctgcata caggagaaag agactggcat 240
 ttgggtcagg gagtctccat agaattggagg aaaaggagat atagcacaca cgtagaccct 300
 gatctagcag accaactaat tcactgtat tattttgatt gttttcaga atctgctata 360
 agaaaagcca tattaggaca cagagttagt ctaggtgtg aatctcgagc aggacatagc 420
 aaggtaggat cactacagta ctggcaata gcagcattaa taacaccaa aaagataaag 480
 ccacctttgg cgagtgtcag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
 aagggccaca gagggagcca tacaatgaat ggacactag 579

<210> 33
 <211> 579
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 33

atggaaaaca gatggcaggt gatgattgtg tggcaggtag acaggatgag gattagaaca 60
 tggaaacagtt tagtaaaata ccatatgtat agatcaaaga aagctaggga atggtttat 120
 agacatcact atcaaaagtc tcatccaaaa gtaagttcag aagtacacat cccactagag 180
 gatgctgatg ttgtaataac aacatattgg ggtctgcata caggagaaag agactggcat 240
 ttgggtcagg gagtctccat agaattggagg aaaaggagat atagcacaca agtagaccct 300
 gatctagcag accacctaatt tcactgtat tattttgatt gttttcaga atctgctata 360
 agaaaagcca tattaggaca cagagttagt ctaggtgtg aatctcgagc aggacatagc 420
 aaggtaggat cactacagta ctggcaata gcagcattaa taacaccaa aaagataaag 480
 ccacctttgg cgagtgtcag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
 aagggccaca gagggagcca tacaatgaat ggacactag 579

<210> 34
 <211> 579
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 34

atggaaaaca gatggcagggt gatgattgtg tggcaggtag acaggatgag gattagaaca 60
 tggaacagtt tagtaaaata ccatatgtat agatcaaaga aagctaggga atggtttat 120
 agacatcact atcaaagttcc tcatccaaa gtaagttcag aagtacacat cccactagag 180
 gatgctagat tggtaataac aacattttgg ggtctgcata caggagaaaag agactggcat 240
 ttgggtcagg gagtctccat agaattggagg aaaaggagat atagcacaca cgtagaccct 300
 gatctagcag accaactaat tcatctgtat tattttgatt gttttcaga atctgctata 360
 agaaaaacca tattaggaca cagagttagt cctaggtgtg aatatcgagc aggcacatagc 420
 aaggttagat cactacagta ctggcaata gcagcattaa taacacaaa aaagataaag 480
 ccacctttgc cgagtgtcag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
 aagggtcaca gagggagcca tacaatgaat ggacactag 579

<210> 35

<211> 579

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 35

atggaaaaca gatggcagggt gatgattgtg tggcaggtag acaggatgag gattagaaca 60
 tggaacagtt tagtaaaata ccatatgtat agatcaaaga aagctaggga atggtttat 120
 agacatcact atcacctgcc tcatccaaa gtaagttcag aagtcacat cccactagag 180
 gatgctagat tggaaataac aacattttgg ggtctgcata caggagaaaag agactggcat 240
 ttgggtcagg gagtctccat agaattggagg aaaaggagat atagcacaca agtagaccct 300
 gatctagcag accaactaat tcatctgtat tattttgatt gttttcaga atctgctata 360
 agaaaaggcca tattaggaca cagagttagt cctaggtgtg aatatcgagc aggcacatagc 420
 aaggttagat cactacagta ctggcaata gcagcattaa taacacaaa aaagataaag 480
 ccacctttgc cgagtgtcag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
 aagggccaca gagggagcca tacaatgaat ggacactag 579

<210> 36

<211> 584

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 36

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tggacacggt tagtaaaata ccatatgtat tgatcaaaaga aaagaaagaa agggaaatggt 120
 ttatagaca tcactatcac agccctcatc cagaacaaaag ttcaacagcc cacatccgcg 180
 tagtggatgg tagattggaa aaaatagcag ttggagctct ggatacagga gatggcgtct 240
 ggcacagggg gcatacgagtc tccatagaat ggaggaaaag gagatatagc acacaagtag 300
 accctgatct agtagacca ctaaltcatc tctattattt tgattgtttt tcagaatctg 360
 ctataagaaa agccatatta ggacacagag ttagtcttag gtgtgaatat cgagcaggac 420
 atagcaaggt aggatcacta cagtacttgg caatagcagc attaataaca ccaaaaaaga 480
 taaagccacc ttggccgagt gtcaggaaac tgacagagga tagatggaac aagcccaga 540
 agaccaaggg ccacagaggg agccatacaa tgaatggaca ctac 584

<210> 37

<211> 579

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 37

atggaaaaa gatggcaggt gatgattgtg tggcaagtag acaggatgag gattagaaca 60
 tggacacggt tagtaaaaca ccatatgtat gttcaaaaga aagctaagaa atggtttat 120
 agacatcact atgaaagccc tcattccaaa gtaagttcaa cagcccatat cccgtaggg 180
 gatgtagat tggagaaaac agcagtttgg agtctgcagg caggagatgg agtctggcac 240
 agggggcctc cagtctccat agaattggagg aaaaggagat atagcacaca agtagacct 300
 gatttgtag accaactaat tcattctgtat tattttgatt gttttcaga atctgctata 360
 agaaaagcca taitaggata tagagttiagt cctagggtg aataccaagc aggacataat 420
 aagtagggat ctctacagta ctggcacta gcacattaa taacaccaa gaagataaag 480
 ccactttgc ctagtgttag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
 aaggccaca gagggagcca tacaatgaat ggacactag 579

<210> 38

<211> 579

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 38

atggaaaaa gatggcaggt gatgattgtg tggcaagtag acaggatgag gattagagca 60
 tggacacggt tagtaaaaca ccatatgtat gttcaaaaga aagctaggac atggtttct 120
 agacatcact atggaagccc tcattccaaa gtatgttcag aagtacacat cccactaggg 180
 gatgctagat tgggtataac aacataatgg agtctgcatg caggagaatg agactggcat 240
 gtgggtcaga gagtctccat agaattggagg aaaaggagat atagcacaca agtagacct 300
 gacttggcag accaactaat tcattctgtat tattttgatt gttttcaga atctgctata 360

agaaaagcca tattaggata tagagttagt ctaggtgtg aataccaagc aggacataat 420
 aaggtaggat ctctacagta ctggcacta gcagcattaa taacaccaa gaagataaag 480
 ccactttgc ctagtgtgag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
 aagggccaca gaggggagcca tacaatgaat ggacactag 579

<210> 39

<211> 579

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 39

atggaaaaca gatggcaggt gatgattgtg tggcaagtag acaggatgag gattagagca 60
 tggaaacagt tagtaaaaca ccatatttat tttcaaaga aagctaagaa atgggtttat 120
 agacatcact atgaaagccc tcatccaaac gtaagttcag aagtacacat cccactaggg 180
 gatgctagat tggtagacaac accatattgg ggtctgcatg gaggagaaa agactggtat 240
 ctggctcagg gagtctccat agaattggagg aaaaggagat atagcacaca agtagacct 300
 gacctggcag accaactaat tcatctgtat tattttgatt gttttcaga atctgctata 360
 agaaaagcca tattaggata tagagttagt ctaggtgtg aataccaagc aggacataat 420
 aaggtaggat ctctacagta ctggcacta gcagcattaa taacaccaa gaagataaag 480
 ccactttgc ctagtgtgag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
 aagggccaca gaggggagcca tacaatgaat ggacactag 579

<210> 40

<211> 579

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 40

atggaaaaca gatgggaggt gatgattgtg tgggaagtag acaggatgag gattagagca 60
 tggaaacagt tagtaaaaca ccatatgtat gtttcaaaga aagctaagaa atgggtttat 120
 agacatcact atgaaagccc tcatccaaa gtaagttcag aagtacacat cccactaggg 180
 gatgctagat tggtagatac aacatattgg ggtctgcatg caggagaaa agactggcat 240
 ttggctcagg gagtctccat agaattggagg aaaaggagat atagcacaca agtagacct 300
 gacctggcag accaactaat tcatctgtat tattttgatt gttttcaga atctgctata 360
 agaaaagcca tattaggata tagagttagt ctaggtgtg aataccaagc aggacataat 420
 aaggtaggat ctctacagta ctggcacta gcagcattaa taacaccaa gaagataaag 480
 ccactttgc ctagtgtgag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
 aagggccaca gaggggagcca tacaatgaat ggacactag 579

<210> 41
 <211> 579
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 41

atggaaaaca gatggcaggt gatgattgtg tggcaagtag acaggatgag gattagagca 60
 tggaaacagtt tagtaaaaca ccatatgtat gtttcaaaga acgctaagaa atggttttat 120
 cgacatcact atgacagccc tcattccagtc caaagttcaa cagcccatat cccgctaggg 180
 gatggtatgat tgcagaaaaat agcattttgg agtctggatg caggagaaaag agactggcat 240
 ttgggtcagg gagtctccat agaattggagg aaaaggagat atagcacaca agtagacct 300
 gacctggcag accaactaat tcattctgtat tattttgatt gttttcaga atctgctata 360
 agaaaaacca tattaggata tagagttagt cctagggtgtg aataccaagc aggacataat 420
 aaggttaggat ctctacagta ctggcacta gcagcattaa taacaccaa gaagataaag 480
 ccacctttgc ctagtgtgag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
 aaggggcaca gaggaggcca tacaatgaat ggacactag 579

<210> 42
 <211> 579
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 42

atggaaaaca gatggcaggt gatgattgtg tggcaagtag acaggatgag gattagagca 60
 tggaaacagtt tagtaaaaca ccatatgtat gtttcaaaga aagctaagaa atggttttat 120
 agacatcact atgacagccc tcattccaaa gtaagttcag aagtacatat cccactaggg 180
 gatgctgat tggagataac aacatatgg ggtctgcatg caggagaaaag agactggcat 240
 ttgggtcagg gagtctccat agaattggagg aaaaggagat atagcacaca cgtagacct 300
 gacctggcag accaactaat tcattctgtat tattttgatt gttttcaga atctgctata 360
 agaaaaacca tattaggata tagagttagt cctagggtgtg aataccaagc aggacataat 420
 aaggttaggat ctctacagta ctggcacta gcagcattaa taacaccaa gaagataaag 480
 ccacctttgc ctagtgtgag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
 aaggggcaca gaggaggcca tacaatgaat ggacactag 579

<210> 43
 <211> 579
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 43

atggaaaaca gatggcaggt gatgattgtg tggcaagtag acaggatgac gattagagca 60
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 agacatcact atgaaagccc tcatccaaaa gtaagttcag aagtacacat cccactaggg 180
 gatgctagat tgggataaac aacatattgg ggtctgcatg caggagaaag agactggcat 240
 ttgggtcagg gagtctccat agaattggagg aaaaggagat atagcacaca agtagaccct 300
 gacttggcag accaactaac tcatctgtat tattttgatt gttttcaga atctgctata 360
 agaaaagcca tattaggata tagagttagt cctagggtgtg aataccaagc aggacataat 420
 aaggtaggat ctctacagta ctggcacta gcagcattaa taacacaaa gaagataaag 480
 ccacctttgc ctagtgtgag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
 aagggccaca gagggagcca tacaatgaat ggacactag 579

<210> 44

<211> 578

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 44

atggaaaaca gatggcaggt gatgattgtg tggcaagtag acaggatgag gattagagca 60
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 agacatcact atgaccgccc tcatccaaaa gtaagttcag aagtccacat cccactaggg 180
 gatgctagat tggagataaac aacattttgg ggtctgcatg caggagaaag agactggcat 240
 ttgggtcagg gagtctccat agaattggagg aaaaggagat atagcacaca agtagaccct 300
 gacttggcag accaactaac tcatctgtat tattttgatt gttttcaga atctgctata 360
 agaaaagcca tattaggata tagagttagt cctagggtgtg aataccaagc aggacataat 420
 aaggtaggat ctctacagta ctggcacta gcagcattaa taacacaaa gaagataaag 480
 ccacctttgc ctagtgtgag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
 aagggcacag agggagccat acaatgaatg gacactag 578

<210> 45

<211> 579

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 45

atggaaaaca gatggcaggt gatgattgtg tggcaagtag acaggatgag gattagagca 60

tggaaacagtt tagtaaaaca ccatatgttt gtttcaaaga aagctaagaa atggttttat 120
 agacatcact atgaaagccc tcatccaaaa gtaagttcag aagtacacat cccactaggg 180
 gatgctagat tggagataac aacattttgg ggtctgcatg caggagaaa agactggcat 240
 ttgggtcagg gagtctccat agaattggagg aaaaggagat atagcacaca agtagaccct 300
 gacctggcag accaactaat tcatctgtat tattttggtt gttttcaga atctgctata 360
 agaaaagcca tattaggata tagagttagt cctaggtgtg aataccaagc aggacataat 420
 aaggtaggat ctctacagta ctgggacta gcagcattaa taacaccaa gaagataaag 480
 ccacctttgc ctagtgtgag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
 aagggccaca gagggagcca tacaatgaat ggacactag 579

<210> 46

<211> 579

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Novel Sequence

<400> 46

atgaaaaca gatggcaggt gatgattgtg tggcaagtag acaggatgag gattagagca 60
 tggaaacagtt tagtaaaaca ccatatgtat gtttcaaaga aagctaagaa atggttttat 120
 agacatcact atgaaagccc tcatccaaa gtaagttcag aagtacacat cccactaggg 180
 gatgctagat tggagataac aacattttgg ggtctgcatg caggagaaa agactggcat 240
 ttgggtcagg gagtctccat agaattggagg aaaaggagat atagcacaca agtagaccct 300
 gacctggcag accaactaat tcatctgtat tattttgatt gttttcaga atctgctata 360
 agaaaagcca tattaggata tagagttagt cctaggtgtg aataccaagc aggacataat 420
 aaggtaggat ctctacagta ctggcacta gcagcattaa taacaccaa gaagataaag 480
 ccacctttgc ctagtgtgag gaaactgaca gaggatagat ggaacaagcc ccagaagacc 540
 aagggccaca gagggagcca tacaatgaat ggacactag 579